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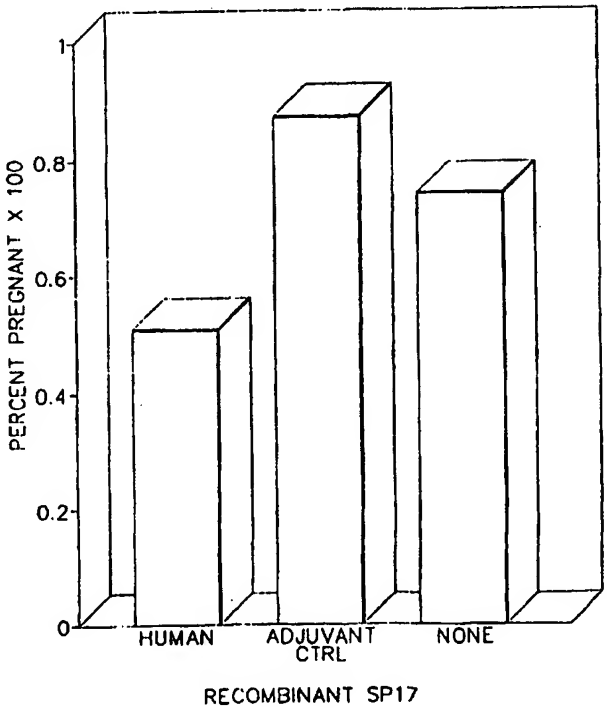
(57) Abstract

The present invention involves antigenic peptides of human Sp17 protein, or antigenic peptides which are fragments thereof. These proteins and peptides are useful as immunocontraceptive agents.



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ANTIGENIC SEQUENCES OF A SPERM PROTEIN AND IMMUNOCONTRACEPTIVE METHODS

This invention was made with Government Support under Grant No. U54 HD29009 from the National Institutes of Health. The Government has certain rights to this invention.

Field of the Invention

The present invention relates to antigens which correspond to autoantigenic epitopes on a sperm zona pellucida binding protein, along with immunocontraceptive methods employing the same.

Background of the Invention

Autoantigens are tissue components of an organism to which that organism directs an immune response. The condition which results from such a self-directed immune response is known as autoimmunity (or "autoallergy"). Proteins in or on sperm are known to be potent autoantigens, and autoimmunity to such proteins is believed a significant cause of infertility.

R. Shabanowitz and M. O'Rand, *Ann. NY Acad. Sci.* **541**, 621-632 (1988), at **Figure** 7, describes various human proteins which have affinity for human zona pellucida.

M. O'Rand and E. Widgren, U.S. Patent No. 5,175,148, discloses a sperm antigen which corresponds to an autoantigenic epitope of Rabbit Sperm Membrane Autoantigen (RSA). RSA is now known to be a family of four low molecular weigh glycoproteins (RSA-1,2,3,4: 14K, 16K, 17K, 18K) which function as high affinity zona binding proteins. The cloning of rabbit RSA 3 (also called "sp17") is described in R. Richardson and M. O'Rand, *Mol. Biol. Cell.* 3, 15a (1992).

Summary of the Invention

A first aspect of the present invention is an antigenic peptide having an amino acid sequence according to SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:128, SEQ ID NO:233 or SEQ ID NO:234, or fragments thereof which are at least six amino acids in length.

A further aspect of the present invention is an immunocontraceptive method comprising administering one of the above peptides, or a combination thereof, to a subject in an amount effective to reduce fertility.

A further aspect of the present invention is an immunocontraceptive vaccine formulation comprising one or more of the above peptides in combination with a pharmaceutically acceptable carrier.

Brief Description of the Drawings

Figure 1 shows the binding of antiserum from a male rabbit injected with his own sperm to the rabbit Sp17 sequential decapeptides having the amino acid sequences disclosed herein as SEQ ID NO:3 through SEQ ID NO:49. In this figure, the SEQ ID NO for each decapeptide is given to the left and/or right thereof.

Figure 2 shows the binding of a pool of sera from four vasectomized men with high titers of antisperm antibodies, tested against the rabbit Sp17 sequential decapeptides used in **Fig 1**. All the peaks on this graph represent human autoantigenic, B-cell epitopes.

Figure 3 shows the binding of immune sera from a female rabbit immunized with rabbit Sp17 recombinant antigen to the sequential decapeptides described in **Fig. 1**.

Figure 4 shows the binding of immune sera taken from a male rabbit immunized with the synthetic peptide G22C (SEQ ID NO:61) to the sequential decapeptides described in **Fig. 1**.

Figure 5 shows the binding of immune sera taken from a female rabbit immunized with the synthetic peptide G22C to the sequential decapeptides described in **Fig. 1.**

Figure 6 illustrates the effect of immunization of mice with recombinant Sp17 (fusion protein) on fertility. Six mice received human Sp17. Adjuvant controls (n=12) received TITERMAX™ adjuvant (available from Sigma Co., St. Louis) only. Six mice received no injections.

Figure 7 gives the alignment of the rabbit (RABSP17), mouse (MUSSP17), and human (HUMSP17) Sp17 protein sequences. Autoantigenic fragments are indicated in the boxes. Numbering is from N-terminus to C-terminus, based on the numbering of the human sequence, with gaps introduced into the other mammalian sequences to maximize alignment of the autoantigenic fragments shown in the boxes, and numbers skipped where gaps are introduced so that the numbering of the autoantigenic fragments indicated in the boxes corresponds across species.

Figure 8 gives the alignment of the baboon (BABSP17), human (HUMSP17), rabbit (RABSP17) and mouse (MUSSP17) Sp17 protein sequences. Numbering of amino acids is from N-terminus to C-terminus, based on the numbering of the aligned sequences, with gaps introduced into the sequences to maximize alignment.

Figure 9 is a mimotope analysis of sera from female mice immunized with recombinant hSP17, using the mouse sequence mimotope plate. "Z score" is the individual peptide pin reactivity minus the mean reactivity for all peptide pins, divided by the standard deviation for the antiserum used.

Figure 10 is a mimotope analysis of sera from female mice immunized with peptide A9DT (SEQ ID NO:138), containing a nine base pair sequence from the human Sp17 sequence, with T-cell epitope synthesized as the initial part of the peptide.

Figure 11 graphically displays the fertility of mice immunized with peptides A9DT (SEQ ID NO:138), V9HT (SEQ ID NO:137) and G9GT (SEQ ID NO:136). Only immunization with A9DT provided a significant decrease in percentage of mice becoming pregnant (33%) and in number of pups in each pregnancy (average 1.9 pups/mouse).

Figure 12 is a mimotope analysis (using decapeptides of human Sp17) of serum from baboons immunized with human recombinant Sp17 (SEQ ID NO:65); this figure is typical of that obtained in each of three test baboons.

Figure 13 graphs the reactivity of sera obtained from human subjects known to contain anti-sperm antibody, to human recombinant Sp17. Subjects 1-5 were vasectomized (vx); subjects 6-7 were non-vasectomized; subject 9 was a male control (no anti-sperm antibodies); subject 10 was a female control (no anti-sperm antibodies).

Figure 14A is a mimotope analysis of the reaction to human Sp17, of serum from an infertile male patient after vasovasostomy (surgical reversal of vasectomy).

Figure 14B is a mimotope analysis of the reaction to human Sp17, of serum from an infertile male patient with after vasovasostomy.

Figure 14C is a mimotope analysis of the reaction to human Sp17, of serum from a fertile male patient after vasovasostomy.

Figure 14D is a mimotope analysis of the reaction to human Sp17, of serum from a fertile male patient after vasovasostomy.

Figure 15 is a graph showing binding of recombinant human Sp17 to human zona (closed circles) and pig zona (open triangles).

Figure 16A provides the complete nucleotide sequence of the longest baboon Sp17 cDNA clone obtained, and the deduced amino acid sequence of the open reading

frame. The polyadenylation signals AATAAA are underlined. The start codon ATG is designated by (+1), while the stop codon TAA is shown by (***). An internal *Eco*R I sequence GAATTC is shown in bold, while the mRNA degradation signal sequence ATTTA is shown by arrows.

Figure 16B provides an alternative 3' UTR sequence found in a baboon Sp17 cDNA clone. The polyadenylation signals AATAAG are underlined.

Figure 16C provides an additional alternative 3' UTR sequence found in a baboon Sp17 cDNA clone. The polyadenylation signals AATAAC are underlined

Figure 17A graphs reactivity to recombinant HSp17 in sera samples obtained from ten male subjects pre- and post-vasovasostomy, compared to sera from female (F) and vasectomized male (M) controls.

Figure 17B graphs reactivity to recombinant HSp17 in sera samples obtained from five male subjects pre- and post-vasovasostomy, compared to sera from female (F) and vasectomized male (M) controls.

Figure 18 is the Z score analysis of a mimotope assay of serum from subject 22 at a 1:200 dilution. Significant antibody binding (Z score $\geq$ 2) is shown at peptides PFS-GNL (SEQ ID NO:238) and at peptide AVK-FRG (SEQ ID NO:127).

Detailed Description of the Invention

Amino acid sequences disclosed herein are presented in the amino to carboxy direction, from left to right. The amino and carboxy groups are not presented in the sequence. Nucleotide sequences are presented herein by single strand only, in the 5' to 3' direction, from left to right. Nucleotides and amino acids are represented herein in the manner recommended by the IUPAC-IUB Biochemical Nomenclature Commission, or (for amino acids) by three letter code, in accordance with 37 CFR §1.822 and established usage. *See, e.g.*, PatentIn User Manual, 99-102 (Nov. 1990)(U.S. Patent and Trademark

Office, Office of the Assistant Commissioner for Patents, Washington, D.C. 20231); U.S. Patent No. 4,871,670 to Hudson et al. at Col. 3 lines 20-43 (applicants specifically intend that the disclosure of this and all other patent references cited herein be incorporated herein by reference).

A. Molecular Biology

DNAs which encode human Sp 17 proteins, whether they are cDNAs or genomic DNAs, encode a protein of about 17 Kilodaltons which binds to human zona pellucida at high affinity by binding sulfated, complex carbohydrates. This definition is intended to encompass natural allelic variations in the DNAs.

DNAs encoding Sp 17 proteins which hybridize to the DNA encoding the human Sp 17 protein disclosed herein, may be of any species of origin, including murine (mouse, rat), rabbit, cat, porcine, human, monkey, or baboon, but preferably code for an Sp 17 protein of mammalian origin, and most preferably code for human Sp 17 proteins. Synthetic DNAs may be made in accordance with known techniques.

Hybridization conditions which will permit other DNA sequences which code on expression for an Sp 17 protein to hybridize to a DNA sequence as given herein are, in general, high stringency conditions. For example, hybridization of such sequences may be carried out under conditions represented by a wash stringency of 0.3 M NaCl, 0.03 M sodium citrate, 0.1% SDS at 60°C or even 70°C to DNA disclosed herein (e.g., SEQ ID NO:1) in a standard in situ hybridization assay. (*See* J. Sambrook et al., Molecular Cloning, A Laboratory Manual (2d Ed. 1989)(Cold Spring Harbor Laboratory)).

In general, DNA sequences which code for Sp 17 proteins and hybridize to the DNA sequence encoding the human Sp 17 protein disclosed herein will be at least 70%, 75%, 80%, 85%, 90%, or even 95% homologous or more

with the sequence of the DNA encoding the human Sp 17 protein disclosed herein.

In general, DNA sequences which encode human Sp 17 proteins which hybridize to the DNA encoding the human Sp 17 protein disclosed herein will be 93%, 94%, 95%, 96%, or even 97% homologous or more to the DNA sequence encoding the human Sp 17 protein disclosed herein.

Further, DNA sequences which code for the same Sp 17 protein as coded for by the foregoing sequences, but which differ in codon sequence from these due to the degeneracy of the genetic code, are also an aspect of this invention. The degeneracy of the genetic code, which allows different nucleic acid sequences to code for the same protein or peptide, is well known in the literature. *See e.g.*, U.S. Patent No. 4,757,006 to Toole et al. at Col. 2, **Table 1**.

The production of cloned genes, recombinant DNA, vectors, transformed host cells, proteins and protein fragments by genetic engineering is well known. See, e.g., U.S. Patent No. 4,761,371 to Bell et al. at Col. 6 line 3 to Col. 9 line 65; U.S. Patent No. 4,877,729 to Clark et al. at Col. 4 line 38 to Col. 7 line 6; U.S. Patent No. 4,912,038 to Schilling at Col. 3 line 26 to Col. 14 line 12; and U.S. Patent No. 4,879,224 to Wallner at Col. 6 line 8 to Col. 8 line 59.

A vector is a replicable DNA construct. Vectors are used herein either to amplify DNA encoding Sp 17 proteins as given herein and/or to express DNA which encodes Sp 17 proteins as given herein. An expression vector is a replicable DNA construct in which a DNA sequence encoding a Sp 17 protein is operably linked to suitable control sequences capable of effecting the expression of the DNA sequence in a suitable host. The need for such control sequences will vary depending upon the host selected and the transformation method chosen. Generally, control sequences include a transcriptional promoter, an optional operator sequence to control

transcription, a sequence encoding suitable mRNA ribosomal binding sites, and sequences which control the termination of transcription and translation. Typical vectors include, but are not limited to, plasmids, viruses, phage, and integratable DNA fragments (i.e., fragments integratable into the host genome by recombination).

DNA regions are operably linked or operably associated when they are functionally related to each other. For example, a promoter is operably linked to a coding sequence if it controls the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to permit translation.

Transformed host cells are cells which have been transformed or transfected with vectors containing a DNA sequence as disclosed herein constructed using recombinant DNA techniques. Transformed host cells ordinarily express the receptor, but host cells transformed for purposes of cloning or amplifying the receptor DNA do not need to express the receptor.

Suitable host cells include prokaryote, yeast or higher eukaryotic cells such as mammalian cells and insect cells. Cells derived from multicellular organisms are a particularly suitable host for recombinant Sp 17 protein synthesis, and mammalian cells are particularly preferred. Propagation of such cells in cell culture has become a routine procedure (Tissue Culture, Academic Press, Kruse and Patterson, editors (1973)). Examples of useful host cell lines are VERO and HeLa cells, and Chinese hamster ovary (CHO) cell lines. Expression vectors for such cells ordinarily include (if necessary) an origin of replication, a promoter located upstream from the DNA encoding the Sp 17 protein to be expressed and operatively associated therewith, along with a ribosome binding site, an RNA splice site (if

intron-containing genomic DNA is used), a polyadenylation site, and a transcriptional termination sequence.

The transcriptional and translational control sequences in expression vectors to be used in transforming vertebrate cells are often provided by viral sources. For example, commonly used promoters are derived from polyoma, Adenovirus 2, and Simian Virus 40 (SV40). See, e.g., U.S. Patent No. 4,599,308.

An origin of replication may be provided either by construction of the vector to include an exogenous origin, such as may be derived from SV40 or other viral source (e.g. Polyoma, Adenovirus, VSV, or BPV), or may be provided by the host cell chromosomal replication mechanism. If the vector is integrated into the host cell chromosome, the latter is often sufficient.

Rather than using vectors which contain viral origins of replication, one can transform mammalian cells by the method of cotransformation with a selectable marker and the receptor DNA. Examples of suitable selectable markers are dihydrofolate reductase (DHFR) or thymidine kinase. This method is further described in U.S. Pat. No. 4,399,216.

Host cells such as insect cells (e.g., cultured *Spodoptera frugiperda* cells) and expression vectors such as the baculovirus expression vector may be employed in carrying out the present invention, as described in U.S. Patents Nos. 4,745,051 and 4,879,236 to Smith et al.

Prokaryote host cells include gram negative or gram positive organisms, for example *Escherichia coli* (*E. coli*) or *Bacilli*.

Eukaryotic microbes such as yeast cultures may also be transformed with vectors carrying the isolated DNAs disclosed herein. see, e.g., U.S. Patent No. 4,745,057. *Saccharomyces cerevisiae* is the most commonly used among lower eukaryotic host microorganisms, although a number of other strains are commonly available.

B. Peptides

One group of exemplary antigenic fragments of the present invention, useful in immunocontraceptive methods, are peptides having an amino acid sequence selected from the group consisting of SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:128, SEQ ID NO:233, and SEQ ID NO:234. Also useful are fragments of the above antigenic peptides which are at least six amino acids in length and which are themselves antigenic.

A further group of exemplary antigenic fragments of the present invention, illustrated by **Figure 1** herein, are antigenic fragments selected from the group consisting of peptides having the amino acid sequence given herein as: SEQ ID NO:3, SEQ ID NO;4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:34, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:43, and fragments thereof which are at least six amino acids in length. Of these, particularly preferred are antigenic fragments selected from the group consisting of peptides having the amino acid sequence given herein as: SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:43, and fragments thereof which are at least six amino acids in length.

Another group of exemplary antigenic fragments of the present invention, illustrated by **Figure 2** herein, are antigenic fragments selected from the group consisting of peptides having the amino acid sequence given herein as: SEQ ID NO;3, SEQ ID NO;6, SEQ ID NO;7, SEQ ID NO;8, SEQ ID NO;9, SEQ ID NO;10, SEQ ID NO;11, SEQ ID NO;12, SEQ ID NO;13, SEQ ID NO;14, SEQ ID NO;15, SEQ

ID NO;16, SEQ ID NO;17, SEQ ID NO;20, SEQ ID NO;21, SEQ ID NO;22, SEQ ID NO;23, SEQ ID NO;24, SEQ ID NO;25, SEQ ID NO;26, SEQ ID NO;27, SEQ ID NO;28, SEQ ID NO;29, SEQ ID NO;30, SEQ ID NO;32, SEQ ID NO;33, SEQ ID NO;34, SEQ ID NO;35, SEQ ID NO;36, SEQ ID NO;38, SEQ ID NO;39, SEQ ID NO;40, SEQ ID NO;43, SEQ ID NO;47, SEQ ID NO;48, SEQ ID NO;49, and fragments thereof which are at least six amino acids in length. Of these, particularly preferred are antigenic fragments selected from the group consisting of peptides having the amino acid sequence given herein as: SEQ ID NO;8, SEQ ID NO;9, SEQ ID NO;14, SEQ ID NO;15, SEQ ID NO;16, SEQ ID NO;21, SEQ ID NO;22, SEQ ID NO;24, SEQ ID NO;25, SEQ ID NO;34, SEQ ID NO;40, SEQ ID NO;43, and fragments thereof which are at least six amino acids in length.

Another group of exemplary antigenic fragments of the present invention, as illustrated by **Figures 12, 14A-14D** and **Tables 1-5** herein, are antigenic fragments comprising continuous segments of the human Sp17 amino acid sequence, including those selected from the group consisting of peptides having the amino acid sequence given herein as: SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, NO:110, SEQ ID NO:111, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:191,

SEQ ID NO:192, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230 and fragments thereof which are at least six amino acids in length.

In general, longer peptides preferably include the sequence of an antigenic peptide as described above. Longer peptides provide the antigenic sequence in an exposed position on the molecule, and not buried in the interior of the molecule where it would be unavailable for a binding event. Longer peptides which add not more than four additional amino acids to either the N terminal or C terminal of the antigen are preferred because sequences of such length are generally insufficient to provide an additional epitope on the longer peptide which might be detrimental to the activity of the antigen. Longer peptides encompass the sequence of an antigenic peptide as described above within a fragment of the Sp17 protein, the fragment representing a single continuous segment of the Sp17 amino acid sequence. An example of such a longer peptide is a peptide having the sequence KREKTNFDPAEWGSKV (SEQ ID NO:233, consisting of amino acids 49-64 of SEQ ID NO:2), which encompasses both SEQ ID NO:19 and SEQ ID NO:20 and represents a continuous fragment of the amino acid sequence of human Sp17. A further example of such a longer peptide is a peptide having the sequence AVKIQAAFRGHIAREEAKK (SEQ ID NO:234, consisting of amino acids 118-136 of SEQ ID NO:2).

C. Species Specific Antigenic Peptides

Peptides comprising a continuous segment of the amino acid sequence of Sp17 have been found to be antigenic in several mammalian species. The antigenicity of the fragments has been found to vary among species. As evidenced in **Figure 9**, female mice immunized with recombinant human Sp17 developed antibodies which

preferentially bound to specific decapeptides of the Sp17 sequence. As shown in **Figure 10**, mice immunized with a peptide A9DT (SEQ ID No:138, containing the A9D sequence from human Sp17 peptide) produced antibodies which preferentially bound to certain Sp17 decapeptides (SEQ ID NO:106 and SEQ ID NO:107). As shown in **Figure 11**, female mice immunized with peptide A9DT (SEQ ID NO:138) exhibited decreased fertility.

As shown in **Figure 12**, baboons immunized with recombinant human Sp17 (SEQ ID NO:65) developed antibodies which preferentially reacted with specific decapeptides of the human Sp17 sequence.

As shown in **Table 1**, non-human primates immunized with recombinant human Sp17 (SEQ ID NO:65) produced antibodies reactive (Z score $\geq$ 2) to specific decapeptides of human Sp17 sequence. Sequence ID numbers are provided after each decapeptide in **Table 1**. As also shown in **Table 1** sera from vasectomized human males with known anti-sperm antibody titer contained antibodies reactive (Z score $\geq$ 2) to certain decapeptides of human Sp17 sequence.

The results of **mimotope analyses of rHSp17 using sera from 13 subjects are displayed in Table 2, and indicate the native HSp17 linear B cell epitopes. All subjects exhibited comparable patterns of antibody reactivity restricted predominantly to two regions of the molecule: epitopes within peptide PFS-GNL (SEQ ID NO:238) and peptide AVK-FRG (SEQ ID NO:127). While anti-Sp17 reactivity varied among subjects, the most predominant linear B cell epitopes were constant.**

Table 3 provides a summary of human Sp17 decapeptides (1 amino acid shift) from amino acids 40-80 of SEQ ID NO:2, and which contain antigenic epitopes for rabbits, non-human primates, and humans. Sequence ID numbers are provided after each peptide in **Table 3**.

Table 4 provides a summary of human Sp17 decapeptides (1 amino acid shift) from amino acids 114-

149 of SEQ ID NO:2, and which contain antigenic epitopes for rabbits, non-human primates, and humans. Sequence ID numbers are provided after each peptide in **Table 4**.

Table 5 provides a summary of human Sp17 decapeptides found to contain antigenic epitopes in mice, rabbits, non-human primates and humans. Sequence ID numbers are provided after each peptide in **Table 5**.

D. Analogs

Peptides which may be used to carry out the present invention include analogs thereof. As used herein, analogs are those compounds which, while not having amino acid sequences identical to those of the peptides described above, have a similar three-dimensional structure. In protein molecules which interact with a receptor, the interaction between the protein and the receptor must take place at the surface-accessible sites in a stable three-dimensional molecule. By arranging the critical binding site residues in an appropriate conformation, peptides which mimic the essential surface features of the peptides of the present invention are designed and synthesized in accordance with known techniques. Methods for determining peptide three-dimensional structure and analogs thereto are known, and are sometimes referred to as "rational drug design techniques". *See, e.g.*, U.S. Patent No. 4,833,092 to Geysen; U.S. Patent No. 4,859,765 to Nestor; U.S. Patent No. 4,853,871 to Pantoliano; U.S. Patent No. 4,863,857 to Blalock; (applicants specifically intend that the disclosures of all U.S. Patent references cited herein be incorporated by reference herein in their entirety). *See also* Waldrop, *Science*, 247, 28029 (1990); Rossmann, *Nature*, **333**, 392-393 (1988); Weis et al., *Nature*, 333, 426-431 (1988). Techniques for constructing and screening libraries of peptide sequences to identify peptides that specifically bind to a given protein are known. Scott and Smith, *Science*, 249, 386-390 (1990);

Devlin et al., *Science*, 249, 404-406 (1990). Further, those skilled in the art will appreciate that minor deletions or substitutions may be made to the amino acid sequences of peptides of the present invention without unduly adversely affecting the activity thereof. Thus, peptides containing such deletions or substitutions are a further aspect of the present invention.

In peptides containing substitutions or replacements of amino acids, one or more amino acids of a peptide sequence may be replaced by one or more other amino acids which does not affect the antigenicity of that sequence. Such changes can be guided by known similarities between amino acids in physical features such as charge density, hydrophobicity/hydrophilicity, size and configuration, so that amino acids are substituted with other amino acids having essentially the same functional properties. For example:

Ala may be replaced with Val or Ser;

Val may be replaced with Ala, Leu, Met, or Ile, preferably Ala or Leu;

Leu may be replaced with Ala, Val or Ile, preferably Val or Ile;

Gly may be replaced with Pro or Cys, preferably Pro;

Pro may be replaced with Gly, Cys, Ser, or Met, preferably Gly, Cys, or Ser;

Cys may be replaced with Gly, Pro, Ser, or Met, preferably Pro or Met;

Met may be replaced with Pro or Cys, preferably Cys;

His may be replaced with Phe or Gln, preferably Phe;

Phe may be replaced with His, Tyr, or Trp, preferably His or Tyr;

Tyr may be replaced with His, Phe or Trp, preferably Phe or Trp;

Trp may be replaced with Phe or Tyr, preferably Tyr;

Asn may be replaced with Gln or Ser, preferably Gln;

Gln may be replaced with His, Lys, Glu, Asn, or Ser, preferably Asn or Ser;

Ser may be replaced with Gln, Thr, Pro, Cys, or Ala;

Thr may be replaced with Gln or Ser, preferably Ser;

Lys may be replaced with Gln or Arg;

Arg may be replaced with Lys, Asp or Glu, preferably Lys or Asp;

Asp may be replaced with Lys, Arg, or Glu, preferably Arg or Glu; and

Glu may be replaced with Arg or Asp, preferably Asp.

Once made, changes can be routinely screened to determine their effects on antigenicity with antibodies which bind to the antigen.

The term "antigenic equivalents" as used herein, refers to proteins or peptides which bind to an antibody which binds to the protein or peptide with which equivalency is sought to be established. Antibodies which are used to select such antigenic equivalents are referred to as "selection antibodies" herein. Antigenic equivalents may be formed by modifying reactive groups within a natural sequence or modifying the N-terminal animo and/or C-terminal carboxyl group. Such equivalents include salts formed with acids and/or bases, particularly physiologically acceptable inorganic and organic acids and bases. Other equivalents include modified carboxyl and/or amino groups on the antigen to produce esters or amides, or amino acid protecting groups such a N-t-butoxycarbonyl. Preferred modifications are those which provide a more stable, active peptide which will be less prone to enzymatic degradation in vivo.

C. Immunocontraceptive Methods

As noted above, the present invention provides an immunocontraceptive method comprising administering an animal subject an antigen as described above in an amount effective to reduce the fertility of that subject. Partial reductions in fertility (i.e., effects which are reflected as a reduction in fertility in a population of subjects) are intended as within the scope of the present invention.

Any animal may be treated by the immunocontraceptive method of the present invention, including both birds and mammals. Exemplary mammals include mice, rabbits, dogs, cats, cows, pigs, sheep, horses and humans. Mammalian subjects are preferred. The subject may be male or female. The antigen may be administered to the subject by any suitable means. Exemplary are by intramuscular injection, by subcutaneous injection, by intravenous injection, by intraperitoneal injection, by oral administration, and by nasal spray.

As noted above, antigenic epitopes of Sp17 vary among mammalian species. Thus the peptide administered as an immunocontraceptive is preferably one known to be antigenic for the species being treated. As illustrated herein, antigenic epitopes of Sp17 may be determined by one skilled in the art on a species-specific basis using mimotope analysis, and the ability of an antigenic peptide to act as an immunocontraceptive may also be determined by one skilled in the art using accepted experimental designs. The specific immunocontraceptive peptide to be administered may vary depending on the species of the subject being treated.

The amount of antigen administered will depend upon factors such as route of administration, species, and the use of booster administrations. In general, a dosage of about 0.1 to about 100 μg per pound subject body weight may be used, more particularly about 1 μg per pound.

The immunocontraceptive method of the present invention contemplating both human and veterinary treatments, the antigens of the present invention may be prepared as both human and veterinary vaccine formulations. Vaccine formulations of the present invention comprise the appropriate antigen in a pharmaceutically acceptable carrier. The antigen is included in the carrier in an amount effective to reduce the fertility of the subject being treated. Vaccine formulations may comprise combinations of appropriate antigens. Pharmaceutically acceptable carriers are preferably liquid, particularly aqueous, carriers, such as sodium phosphate buffered saline. The vaccine formulation may be stored in a sterile glass container sealed with a rubber stopper through which liquids may be injected and formulations withdrawn by syringe.

Vaccine formulations of the present invention may optionally contain one or more adjuvants. Any suitable adjuvant can be used, exemplary being aluminum hydroxide, aluminum phosphate, plant and animal oils, and the like, with the amount of adjuvant depending on the nature of the particular adjuvant employed. In addition, the vaccine formulations may also contain one or more stabilizer, exemplary being carbohydrates such as sorbitol, mannitol, starch, sucrose, dextrin, and glucose, proteins such as albumin or casein, and buffers such as alkaline metal phosphate and the like.

D. Diagnostic Methods

The diagnostic methods of the present invention provide a method of diagnosing autoimmune infertility in both male and female subjects. The term "autoimmune" is here used in a generic sense, as the immunity in female subjects is to exogenous sperm.

Any conventional procedure for detecting antibodies can be employed in practicing the diagnostic assay of the present invention, including agglutination

and precipitation reactions, radioimmunoassays, enzyme immunoassays (e.g., U.S. Pat. No. 3,654,090) such as Enzyme-Linked Immunosorbent Assays (ELISA), heterogeneous fluorescent immunoassays (e.g., U.S. Pat. Nos. 4,201,763; 4,171,311; and 3,992,631), and homogeneous (separation-free) immunoassays. See generally *Basic and Clinical Immunology*, 364-73 (J. Fudenberg et al., eds. 3d Ed. 1980), ELISA is preferred.

In a preferred embodiment, serum from a human to be diagnosed is contacted with an antigen as described above so that antibodies in the serum react in solution with the antigen. While the antigen is preferably bound to a solid support, if a homogeneous (separation free) immunoassay is utilized to detect the antibodies, a solid support would not be required.

Serum may be obtained from a person generally pricking a finger and obtaining whole blood (of which serum is a constituent). However, the blood may be processed to obtain only the serum or plasma portion of the whole blood before contacting the serum with the bound antigens. Any method for obtaining serum or plasma from a patient may be utilized as long as the antibodies contained therein retain their ability to bind the antigen.

The antigens may be bound to solid supports by known techniques. For example, a bi-functional organic molecule may be used to attach the antigen to a solid support. The solid can be made of materials such as plastic (e.g., the bottom surface of a well in a microtiter plate), fiberglass, cellulose acetate and nitrocellulose (e.g., discs). After being attached or adhered to the solid support, the antigens can be cross-linked if desired.

The step of contacting the solid support with a detectable antibody is carried out so that the detectable antibody is allowed to interact with the antigen bound to the solid support. The detectable

antibody is one which is capable of binding to a human antibody from the serum of the patient which has bound to the purified antigen, where the detectable antibody is capable of being detected. More particularly, the detectable antibody can be an anti-human immunoglobulin which is conjugated to a group such as an enzyme which is detectable in the presence of a substrate. Enzyme-conjugated goat or rabbit anti-human antibodies which have been affinity purified are preferred. In general, the detectable group which is conjugated to the detectable antibody may be any enzyme or other detectable species which has been developed for immunoassays. For example, enzymes, fluorescent groups, radioactive groups and others could be used. The enzyme peroxidase is particularly preferred. When peroxidase is the detectable group conjugated to the detectable antibody, a substrate such as 3.3', 5.5'-tetramethylbenzidine or o-phenylenediamine may be used as the substrate for detection of the detectable antibody.

The step of detecting the detectable antibody that has reacted with the human antibodies involves treating or manipulating the detectable group which is conjugated to the detectable antibody to determine its presence. For example, if an enzyme such as peroxidase is conjugated to the antibody, the detecting step would involve adding a peroxidase substrate to the bound antibody, and adding a peroxidase substrate to the bound antibody and observing a color change as peroxidase catalyzes conversion of the substrate to a colored species. In the case of other enzymes, such as alkaline phosphatase and β-D-galactosidase, other substrates may be used. The substrate to be used should be chosen such that after the enzyme catalyzes a chemical conversion of the substrate to a product, a change which is observable to a person employing this test should result. Substrates such as 3.3', 5.5'-tetramethylbenzidine, p-nitrophenyl phosphate or 3.3'-diamino-benzidine may be

used as substrates. Other detectable groups may also be conjugated to the antibody.

A kit containing the required components for carrying out a diagnostic test based on detection of serum antibodies can be assembled. The kit comprises a package containing purified antigen coated in or on a solid support such as the bottom of a microtiter plate well or a nitrocellulose or cellulose acetate disc, and a container of a detectable antibody conjugate which is capable of binding antibody from the serum of a patient which is bound to the antigen. An ELISA test is most preferred for the kit since it lends itself to a readily detectable positive or negative diagnosis. Thus, the kit should also house a container of a substrate which is reactive with an enzyme which is conjugated to the detectable antibody, the substrate being readily detectable after reaction with the enzyme. The antigen employed in the diagnostic kit is preferably substantially or essentially free of other proteins.

E. Avirulent Carrier Cells

As noted above, avirulent carrier cells such as microbes are used to administer antigens of the present invention. This method is particularly suitable since appropriate carrier microbes can stimulate production of sIgA to the antigens which they express. Suitable avirulent carrier cells, including both plant carrier cells and microbial carrier cells, are described in R. Curtiss, Vaccines Obtained from Antigenic Gene Products of Recombinant Genes, U.S. Patent No. 4,888,170, R. Curtiss and G. Cardineau, Oral Immunization by Transgenic Plants, PCT Application WO 90/02484, and R. Curtiss, Recombinant Avirulent Salmonella Antifertility Vaccines, PCT Application WO 92/09684, the disclosures of which are incorporated herein by reference.

In general, recombinant plasmids containing one or more genes for the gamete-specific antigens can be

introduced into one of several avirulent strains of bacteria containing mutations for genes necessary for long-term survival in the targeted host. Useful avirulent microbes include, but are not limited to, mutant derivatives of Salmonella and E. coli-Salmonella hybrids. Preferred microbes are members of the genus Salmonella such as S. typhimurium, S. typhi, S. parathyphi, S. gallinarum, S. pullorum, S. enteritidis, S. choleraesuis, S. arizona, or S. dublin. Avirulent derivatives of S. typhimurium and S. enteritidis find broad use among many hosts. Avirulent derivatives of S. gallinarum, S. pullorum and S. arizona may be particularly useful for immunizing avian species whereas S. typhimurium, S. typhi and S. parathyphi are preferred for use in humans. S. choleraesuis is preferably used to immunize swine while S. dublin finds use in cattle.

Particularly useful are one, two or all three of the cya, crp and asd mutants which are substantially incapable of producing the corresponding functional protein in a host, such that growth is impaired. However, other avirulent microbes will also find use with the present invention. Such avirulent microbes include those with aroA, aroD, galE, phoP, cdt, omoR and htrA mutations. If Asd mutants are used, the antigen of interest is transferred to the carrier microbe using a vector encoding both the antigen and asd. Thus, only those carrier microbes containing the desired gamete-specific antigen will survive and these microbes can be selected for further use. Expression of the recombinant gene encoding the desired antigen maybe dependent on a control sequence linked to the asd gene. This linkage may result from the orientation of the two genes in the vector so that both genes could be, for example, under the control of the same control elements, i.e., the same promoter and operator.

The cya mutants and/or crp mutants can be further mutated, preferably by a deletion, in a gene

adjacent to the crp gene which governs virulence of Salmonella. Mutation in this gene, the cdt gene, diminishes the ability of the bacteria to effectively colonize deep tissues, e.g., the spleen. When a plasmid having the crp⁺ gene is placed in a strain with the Δ(crp-cdt), it retains its avirulence and immunogenicity thus having a phenotype similar to cya and crp mutants. Mutants with the Δ(crp-cdt) mutation containing a crp⁺ gene on a plasmid retain the normal ability to colonize the intestinal tract and GALT, but have a diminished ability to colonize deeper tissues.

In order to stimulate a preferred immune response, introduction of the microbe or gene product directly into the gut or bronchus is preferred, such as by oral administration, intranasal administration, gastric intubation or in the form of aerosols, as well as air sac inoculation (in birds only), and intratracheal inoculation. Other suitable methods include administration via the conjunctiva to reach the Harder gland and intramammary inoculation. Other methods of administering the vaccine, such as intravenous, intramuscular, or subcutaneous injection are also possible, and used principally to stimulate a secondary immune response, as described further below.

Generally, when carrier microbes expressing the antigens are administered to humans or other mammals, they will be present in a pharmaceutically acceptable carrier. For example, the carrier microbes can be enteric-coated or encapsulated with a suitable gelatin-like substance, known in the art (Cryz and Glück, 1990, in G. Woodrow and Mr. Levine, New Generation Vaccines, Marcel Dekker, New York, pp. 921-932).

Once the carrier microbe is present in the animal, the antigen must become available to the animal's immune system. This may be accomplished when the carrier microbe dies so that the antigen molecules are released. Of course, the use of "leaky" avirulent mutants that

release the contents of the periplasm without lysis is also possible. Alternatively, a gene may be selected that controls the production of an antigen that will be made available by the carrier cell to the outside environment prior to the death of the cell.

The antigens may also be administered as aerosols or intranasally. Intranasal formulations for human subjects will usually include vehicles that neither cause irritation to the nasal mucosa nor significantly disturb ciliary function. Diluents such as water, aqueous saline or other known substances can be employed with the subject invention. The nasal formulations may also contain preservatives such as but not limited to chlorobutanol and benzalkonium chloride. A surfactant may be present to enhance absorption of the subject proteins by the nasal mucosa.

Injection of the gamete-specific antigen can also be done in conjunction with prior oral, intranasal, gastric or aerosol immunization. Such parenteral immunization can serve as a booster to enhance expression of the secretory immune response once the secretory immune system to the gamete-specific gene product has been primed by immunization with the carrier microbe expressing the gamete-specific gene product. The enhanced response is known as a secondary, booster, or anamnestic response and results in prolonged immune protection of the host. Booster immunizations may be repeated numerous times with beneficial results.

When the vaccines are prepared as injectables, such as for boosters, they can be made either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation may also be emulsified or the active ingredient encapsulated in liposome vehicles. The active immunogenic ingredient is often mixed with vehicles containing excipients which are pharmaceutically acceptable and compatible with the

active ingredient. Suitable vehicles are, for example, water, saline, dextrose, glycerol, ethanol, or the like, and combinations thereof. In addition, if desired, the vehicle may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, or adjuvants which enhance the effectiveness of the vaccine. Adjuvants may include for example, muramyl dipeptides, avridine, aluminum hydroxide, oils, saponins and other substances known in the art. Actual methods of preparing such dosage forms are known, or will be apparent, to those skilled in the art. See, e.g., Remington's Pharmaceutical Sciences, Mack Publishing Company, Easton, PA, 15th ed., 1975. The composition or formulation to be administered will, in any event, contain a quantity of the protein adequate to achieve the desired immunized state in the individual being treated.

The quantity of antigen to be administered depends on the subject to be treated, the capacity of the subject's immune system to synthesize antibodies, and the degree of protection desired. Effective dosages can be readily established by one of ordinary skill in the art through routine trials establishing dose response curves. The subject is immunized by administration of the particular antigen or fragment thereof, or analog thereof, in at least one dose. Typical doses using the carrier microbe are on the order of $1 \times 10^6 - 1 \times 10^{10}$ recombinant avirulent bacteria/immunized subject. The subject may be administered increasing amounts or multiple dosages as required to maintain a state of immunity to the gamete-specific antigen.

It may be desirable to administer more than one antigen simultaneously or consecutively. This can be accomplished either by administering an avirulent carrier containing genes encoding for more than one gamete-specific antigen or by administering different carrier organisms.

The present invention is explained below in the following non-limiting Examples.

EXAMPLE 1

Cloning and Sequencing of Human Sperm Zona Binding Protein Sp17

We have previously reported cloning and sequence data of rabbit Sp17 (Richardson and O'Rand, *Mol. Biol. Cell* 3, 15a (1992)). This protein is known to be a member of the rabbit sperm antigen (RSA) family of rabbit testis/sperm autoantigens and also to be expressed in mice. Further search for a human counterpart of this protein was initiated with screening of a human testis cDNA library using the protein coding region of the rabbit Sp17 gene as a probe. One clone contained a 1287 base pair insert 71% identical to the rabbit Sp17 gene at the nucleotide level, contained an open reading frame of 455 base pairs, and had the sequence given herein as SEQ ID NO:1. This clone encoded a protein of 151 amino acids having the sequence given herein as SEQ ID NO:2 with a calculated molecular weight of 17,534 Da, 76.7% identical to the rabbit Sp17 and 71.8% identical to the mouse Sp17 protein sequence. In particular, the first 44 amino acids are completely identical in the mouse, rabbit and human sequences and have a 43% identity to the human testis cAMP dependent protein kinase type IIα regulatory sub-unit dimer interaction site. Interestingly, comparison of rabbit, mouse and human amino acid sequences has shown that the human Sp17 lacks the single cysteine residue at the center of the molecule which the other sequences possess. Northern blot analysis of a range of mouse, baboon and human tissues revealed a highly restricted pattern of gene expression limited to the testis. Additionally, Northern analysis has revealed evidence of 2 distinct transcript sizes of approximately 1.3 kb and 0.9 kb in the human testis. Antisera to Sp17 recombinant protein (rSp17) has been generated and used

on Western blots of human sperm lysates to demonstrate a predominant immunoreactive protein of 29 KDa. The antigen was localized by immunofluorescence on human spermatozoa with anti-rSp17. In ELISA rSp17 was shown to bind fucoidan with saturation kinetics. Sera from vasectomized men who have anti-sperm antibody titres also shown reactivity to rSp17, indicating that human Sp17 is a human sperm autoantigen.

EXAMPLE 2

Production of Sequential Decapeptides And Immunoassay Procedures

A series of forty-seven N-terminal acetylated sequential decapeptides corresponding to fragments of the rabbit Sp17 protein were synthesized in accordance with known techniques; these decapeptides are disclosed herein as SEQ ID NO:3 through SEQ ID NO:49.

Enzyme-linked immunosorbent assay (ELISA) was carried out in accordance with known procedures (see, e.g., M. O'Rand et. al. *Dev. Biol.* 129, 231 (1988); O'Rand and Widgren, *Reprod. Fertil. Dev.* 6:289 (1994)), as adapted for the MULTIPIN™ system, in accordance with the manufacturer's specifications. (Chiron Mimotopes Pty. Ltd., Clayton, Victoria, 3168 Australia). Control O.D. values of IgG from a normal control subject were subtracted from experimental values in displaying the ELISA data below, in accordance with standard techniques.

EXAMPLE 3

Production of Antibodies to Peptide G22C

The peptide G22C, which corresponds to the fragment of rabbit Sp17 spanning amino acid 61 to amino acid 82 (and having the sequence: GAKVDDRFYNNHAFQEHESEKC; SEQ ID NO:61) was synthesized at the Salk Institute under contract NO1-HD-0-2906 with the NIH in accordance with standard techniques.

Male and female rabbits were immunized with G22C peptide which was conjugated to keyhole limpet hemocyanin (KLH) with the C-terminal Cys amino acid of G22C. Conjugation was carried out with Ellman's reagent, 5,5'-dithio-*bis*-[2-nitrobenzoic acid] obtained from Pierce Scientific in the form of the IMJECT® immunogen conjugation kit. Each rabbit received subcutaneous injection of 300 μg of conjugate in complete Freund's adjuvant followed by an additional 200 μg of conjugate in incomplete Freund's adjuvant three weeks later and a final 100 μg of conjugate in incomplete Freund's adjuvant three weeks later. Conjugate was provided in 100 μl of water diluted 1:1 with adjuvant.

EXAMPLE 4

Binding of Rabbit AutoImmune Sera to Rabbit Sp17 Sequential Decapeptides

A male rabbit was injected with his own sperm to produce autoimmune sera. Specifically, 2 mg of sperm was washed three times in PBS, resuspended in .5 ml of PBS, diluted 1:1 by volume with Freund's complete adjuvant, and injected subcutaneously. A first booster shot was given one month thereafter, a second booster was given an additional two weeks thereafter, a third booster was given an additional two weeks thereafter, and a fourth booster was given an additional three months thereafter. The immune sera was screened by ELISA as described above with the sequential decapeptides (rabbit Sp17) described above. Results are shown in **Figure 1**. Note the clustering of potential autoantigenic epitopes.

EXAMPLE 5

Binding of Pooled Human AutoImmune Sera to Rabbit Sp17 Sequential Decapeptides

Figure 2 shows the binding of a pool of equal volumes of sera from four vasectomized men with high titers of antisperm antibodies tested against the

sequential decapeptides (rabbit sequence) described above by ELISA as described above.

Note that all the peaks on **Figure 2** represent human autoantigenic B-cell epitopes.

EXAMPLE 6

Binding of Sp17-Immunized Rabbit Sera to Rabbit Sp17 Sequential Decapeptides

The binding of immune sera from a female rabbit immunized with recombinant rabbit Sp17 fusion protein to the sequential decapeptides (rabbit Sp17 sequence) described above is shown in **Figure 3.**

The recombinant fusion protein was generated by PCR using the following primers: for the plus strand, 5'-CGCGGATCCATGTCGATTCCATTTTCC-3' (SEQ ID NO:62) which contains a Bam HI site, and for the antisense primer, 5'-CGGGGTACCGCCAGTGCCCTCAATTGT-3' (SEQ ID NO:63), which contains a Kpn I site. The PCR product was directionally cloned into the polylinker region of pQE-30, sequenced to verify integrity of the insert, and bacterially expressed according to the protocol provided by Qiagen Inc. (Chatsworth, CA). Using this system, the recombinant rabbit Sp17 protein (rSp17; SEQ ID NO:64) is expressed minus the first 11 N-terminal amino acids of rabbit Sp17, but with an N-terminal containing the sequence Arg-Gly-Ser, followed by six histidines and Gly-Ser, all of which precede the Sp17 amino acids. The fusion protein was purified from the bacterial lysate by affinity chromatography using the metal chelate adsorbent nickel-NTA-agarose (Qiagen, Inc.). The fusion protein was eluted with 8 M urea, 0.1 M sodium phosphate (monobasic), 0.01 M Tris, pH adjusted to 5.9, and dialyzed against three changes of PBS. 200 μg of protein in .5 ml PBS with 1 mg ADJUPRIME™ adjuvant (Pierce Chemical Co., Rockford, Illinois, USA) was administered subcutaneously. A first booster of 200 μg in the same volume was given three weeks thereafter.

EXAMPLE 7

Binding of G22C-Immunized Rabbit Sera to Rabbit Sp17 Sequential Decapeptides

The binding of immune sera taken from a male rabbit immunized with the synthetic peptide G22C (SEQ ID NO:61) as described in Example 3 above to the sequential decapeptides described above, by ELISA as described above, is shown in **Figure 4**, and the binding of immune sera taken from a female rabbit immunized with the synthetic peptide G22C as described in Example 3 above to the sequential decapeptides described above is shown in **Figure 5.**

EXAMPLE 8

Immunization of Mice with Sp17

The effect of immunization of mice with recombinant human Sp17 (fusion protein) on fertility was studied. Six mice received only mouse Sp17, six received mouse and then rabbit Sp17, six received only human Sp17. Adjuvant controls (n=12) received TITERMAX™ adjuvant (available from Sigma Co., St. Louis) only. Six mice received no injections. The female mice were then placed with a male mouse. The presence of a vaginal plug was used as evidence of mating; only female mice which had evidence of mating were counted in the chart of **Figure 6.** Of the six mice immunized with human Sp17, six were mated and three of the six became pregnant (50%); of the adjuvant control group, seven mice were mated and six of the seven became pregnant (86%); of the control group, four were mated and three became pregnant (75%). Compared to the 86% pregnancy rate in the adjuvant control group, the 50% pregnancy rate in the hSp17 treatment group represented a 42% decrease in pregnancy. Compared to the 75% pregnancy rate in the control group, the pregnancy rate in the treatment group represented a

33% decrease. In contrast, the difference between the adjuvant control and the control group was 13%.

Recombinant human Sp17 (SEQ ID NO:65) was prepared as a fusion protein in essentially the same manner as described above for recombinant rabbit Sp17, except that no N-terminal Sp17 amino acids were deleted from the resulting product. Balb/c mice were immunized with approximately 5 μg of fusion protein in water diluted 1:1 with Freund's complete adjuvant. Four weeks after the first immunization, three more injections of the fusion protein in incomplete adjuvant were given every two weeks.

EXAMPLE 9

Alignment of Mammalian Sp17s

Figure 7 gives the alignment of the rabbit (RABSP17; SEQ ID NO:50), mouse (MUSSP17; SEQ ID NO:51), and human (HUMSP17; SEQ ID NO:2) Sp17 protein sequences. Autoantigenic fragments are indicated in the boxes. Numbering is from N-terminus to C-terminus, based on the numbering of the human sequence, with gaps introduced into the other mammalian sequences to maximize alignment of the autoantigenic fragments shown in the boxes, and numbers skipped where gaps are introduced so that the numbering of the autoantigenic fragments indicated in the boxes corresponds across species.

EXAMPLE 10

Binding of Recombinant Sp17 to Human Zona Pellucida

Biotinylated human recombinant Sp17 (SEQ ID NO:65) was shown to bind to human zona pellucida by ELISA (**Figure 15**). This is the first demonstration of binding of any recombinant mammalian Sp17 to any mammalian zona pellucida. In **Figure 15**, closed circles indicate binding of recombinant human Sp17 to human zone; open triangle indicate binding to pig zona (used as a control).

EXAMPLE 11

Cloning and Sequencing of Baboon Sperm Zona Binding Protein Sp17 (BSp17)

The search for a baboon counterpart of human Sp17 was initiated with screening of a baboon testis cDNA library using the protein coding region of the human Sp17 cDNA as a probe. A clone was identified which contained an ORF giving rise to a protein of 163 amino acids (predicted MW 18.8 kDa), showing 97.4% homology to hSp17, and having the nucleotide sequence given herein as SEQ ID NO:66. The encoded protein of 163 amino acids has the sequence given herein as SEQ ID NO:67. In particular, the first 44 amino acids of BSp17 are identical to that of the mouse, rabbit and human sequences. Comparison of baboon, rabbit, mouse and human amino acid sequences reveals that both the human and baboon Sp17 lack the single cysteine residue found at the center of the rabbit and mouse sequences. **Figure 8**.

Figure 16A-C provides the sequences of three alternatively spliced messages encoding baboon Sp17. **Figure 16A** shows the sequence for the longest clone isolated, and the deduced amino acid sequence thereof. **Figures 16A** and **16B** show alternative 3'-UTR sequences that were isolated.

EXAMPLE 12

Conservation of Sp17 Gene in Mammalian Species

Southern blots of DNA isolated from human, rhesus monkey, rat, mouse, cow, dog, and rabbit, and from chicken and yeast have been probed using the human Sp17 nucleotide sequence as a probe. A conserved Sp17 gene was found in the mammalian subjects; no homologous Sp17 sequence was found in chicken or yeast.

EXAMPLE 13

Localization of Antigenic Epitopes on Live Spermatozoa

Experiments were conducted to localize Sp17 on human spermatozoa. Antigens present on the surface of the spermatozoa during capacitation and subsequent acrosome reaction would be more likely to affect spermatozoa function than those directed against internal proteins. In the following experiments, rabbit antisera to recombinant rabbit Sp17 (rRSp17) and to KLH (Keyhole Limpet Hemocyanin (Sigma Chemical Co., St. Louis, Mo.)) conjugated peptide R22C were prepared by immunization with 200 μg antigen in Titermax adjuvant (Sigma Chemical Co.). Booster injections were given in incomplete Freund's adjuvant at 4 and 6 weeks. Mouse antiserum to peptide K18C was prepared in the same manner with 50μg peptide-KLH conjugate. Peptides R22C and K18C (3 mg) were coupled via the terminal cysteine residue to sulfolink gel (Pierce, Rockford, IL) according to the manufacturer's instructions. HPLC purified (60μg) recombinant HSp17 was coupled via amine groups to reacti-gel (Pierce, Rockford, IL) in 0.05 M sodium borate buffer pH 9.0 according to the manufacturer's instructions. Antisera to be purified were loaded onto 2 ml peptide columns in PBS and left to stand 1 hour at room temperature. Columns were washed with PBS until OD_{280nm} reached baseline (≤ 0.01) following which the bound antibody was eluted with Pierce Immunopure Elution buffer (Pierce, Rockford, IL). Fractions were collected, neutralized with 100 μl 0.5 TrisCl pH 8.5 and those containing protein were pooled, dialyzed against PBS and concentrated. Immunofluorescent staining was performed on capacitated human spermatozoa. Motile spermatozoa were isolated by direct swim up through 1 ml capacitation medium (BWW; Biggers et al., In: Methods of Mammalian Embryology, pp. 86-116, Freeman and Sons, San Francisco, 1971) containing 35 mg/ml human serum albumin (HSA, fraction V powder, Sigma Chemical Company, St. Louis MO),

penicillin (100 U/ml) and streptomycin (100 μg/ml) for 1 hour at 37 °C, 5% CO_2. After centrifugation (400g, 10 minutes), spermatozoa were resuspended in capacitation medium at a concentration of not less than $1x10^6$ cells/assay. Samples exhibiting at least 80% motility were then capacitated a further 3 hours at 37°C, 5% CO_2. Spermatozoa were then washed in PBS, by centrifugation, fixed with 0.5% formaldehyde for 30 minutes at 4°C, washed, resuspended in PBS and a drop dried on a microscope slide.

Fixed labeled spermatozoa were capacitated as before, washed into PBS and fixed with 0.5% formaldehyde for 30 minutes at 4°C. Following this, spermatozoa were washed, resuspended in PBS and a drop dried onto a microscope slide prior to the addition of R22C antibody (1μg affinity purified antibody).

Biotin labelled goat anti rabbit IgG or biotin-labeled goat anti mouse IgG (1:200; 30 minutes) were used for secondary antibody labeling followed by avidin-Texas red (1:200; 30 minutes). Finally, spermatozoa were mounted in Vectashield mounting medium (Vector Laboratories, Burlingame, CA) and viewed.

Initial experiments to localize Sp17 on live capacitated human spermatozoa were performed using affinity purified antiserum to recombinant RSp17. This demonstrated staining of the principal piece of the tail in 53.2% (± 7.23, n=9) of spermatozoa after 4 hours of capacitation (data not shown).

To determine the surface accessibility of the linear B cell epitopes defined in Example 23, additional experiments were performed using affinity purified anti-peptide antibodies directed against the linear peptide sequences R22C (SEQ ID NO:68 with a terminal cysteine residue attached to provide a peptide of sequence RIPQGFGNLL EGLTREILRE QC) and K18C (SEQ ID NO:70 with a terminal cysteine residue attached to provide a peptide of sequence KIQAAFRGHI AREEAKKC; SEQ ID NO:239).

Antibodies raised to the C-terminal peptide sequence K18C were shown to label the principal piece of the tail in the same way as the rRSp17 antiserum discussed above (data not shown). Fluorescence could be competed away by pre-absorbing the antisera (1μg) with 100 μg K18C peptide or 10μg rHSp17.

In contrast, antibodies directed against the R22C peptide did not label spermatozoa either live or formaldehyde fixed (data not shown). The same antiserum was used for Western blot analysis of human sperm lysates. Lysates were prepared using glycerol stored spermatozoa, thawed and pelleted (12,000g, 5 mins.) and washed in PBS. After centrifugation, lipids were removed by two successive chloroform:methanol (2:1) extractions and the pellet air dried. The sperm pellet was resuspended in an equal volume of water and sonicated (1 minute). An equal volume of sample buffer (50mM TrisCl pH 6.8, 1% (w/v) SDS, 1% (w/v) 2-mercaptoethanol) was added, samples boiled for 5 minutes, centrifuged (12,000g, 5 minutes) and loaded onto gels. Protease inhibitors were maintained throughout (pefabloc SC, Boehringer Mannheim, Indianapolis MN, 2mM; aprotinin 0.5 μg/ml and leupeptin 2μg/ml. Western blots were performed as described, Welch et al., *Biol. Reprod.* 43:127 (1990).

Using 100 μg of human sperm lysate and antibodies against the R22C peptide, native Sp17 was detectable as a triplet of proteins 24.5, 22.6 and 22.1 kDa (data not shown). Using antibodies against the peptide sequence K18C or rRSp17, the same triplet of proteins was recognized and in addition, a doublet of immunoreactive proteins at 20 and 19.1 kDa (data not shown). These results suggest that the doublet of proteins may contain the C-terminal but lack the N-terminal of native Sp17. In addition, faint bands are often seen at 53.7 kDa corresponding to HSp17 multimers. To show antibody specificity, 10 μg of anti-K18C was pre-

incubated with 500 μg K18C peptide for 1 hour which removed all antibody binding to the native protein.

EXAMPLE 14

Mimotope Analysis Methods

Mimotope analyses were performed using the peptide pinblock method of Chiron Mimotopes. An Sp17 sequence was divided into overlapping decapeptide, and the decapeptides attached to a block of pins. All peptides underwent N-terminal acetylation. Antisera reactivity was detected by ELISA as in O'Rand and Widgren, *Reprod. Fertil. Dev.* 6:289 (1994).

A series of forty-eight N-terminal acetylated sequential decapeptides corresponding to fragments of the mouse Sp17 protein were synthesized. Sixteen decapeptides were identical to those of the rabbit Sp17 sequence (SEQ ID NOS:3-17, 21); the remaining decapeptides are provided herein as SEQ ID NOS:71-102. A series of forty-eight N-terminal acetylated sequential decapeptides corresponding to fragments of the human Sp17 protein were synthesized. Fifteen decapeptides were identical to those of the rabbit Sp17 sequence (SEQ ID NOS:3-14, 18, 19, 20); the remaining 36 decapeptides are provided herein as SEQ ID NOS:103-135.

Enzyme-linked immunosorbent assay (ELISA) was carried out in accordance with known procedures as described in Example 2, above and in O'Rand and Widgren, *Reprod. Fertil. Dev.* 6:289 (1994).

Z-scores were calculated for each peptide pin as: (individual peptide pin reactivity - mean reactivity for all peptide pins)/(standard deviation for the antiserum used). Pauls JD et al., *Mol. Immunol.* 30:709 (1993).

EXAMPLE 15

Mimotope Analysis of Mouse Anti-human Sp17

Six female mice were immunized with recombinant human Sp17 (SEQ ID NO:65). Mimotope analysis was conducted using a mouse sequential decapeptide plate prepared as described in Example 13 above. Results are shown in **FIGURE 9**. Two peptides produced Z scores greater than two: FDPAEWGAKV (SEQ ID NO:21) and AEWGAKVEDR (SEQ ID NO:74).

Figure 10 shows the mimotope analysis results using six mice immunized with peptide A9DT (SEQ ID NO:138). Peptide A9DT contains a nine amino acid sequence from the rabbit Sp17 sequence coupled with a T-cell epitope (T=NCAYKTTQANK) synthesized as the initial part of the peptide. Chen et al., *J. Immunol.* 147:3672(1991). The T-cell epitope induces a T-cell response in mice of almost all H2 haplotypes. As above, two peptide pins produced Z scores greater than two: FDPAEWGAKV (SEQ ID NO:21) and AEWGAKVEDR (SEQ ID NO:74).

EXAMPLE 16

Fertility of Mice Immunized with Synthetic Peptides

Female mice (six per treatment group) were immunized with either peptide V9HT (SEQ ID NO:137), or A9DT (SEQ ID NO:138), or peptide G9GT (a non-Sp17 sequence which served as a control; SEQ ID NO:136). The female mice were then placed with a male mouse. The presence of a vaginal plug was used as evidence of mating; only female mice which had evidence of mating were counted in **Figure 11**. Of the 18 total mice, only those six mice receiving peptide A9DT (SEQ ID NO: 138) evidenced a statistically significant decrease in both pregnancy rate and number of pups per pregnancy, as compared to the control group receiving peptide 9G9T.

EXAMPLE 17

Inhibition of Mouse In Vitro Fertilization

The ability of serum from mice immunized with Sp17 peptides to inhibit *in vitro* fertilization of mice oocytes was investigated. Oocytes were considered fertilized if cleavage into a two cell embryo occurred.

Using standard *in vitro* fertilization techniques, mouse oocytes were treated *in vitro* with serum (1/50 dilution) from mice immunized with either peptide K13GTT (SEQ ID NO:236); mice immunized with whole mouse Sp17 (SEQ ID NO:51); or mice immunized with peptide A9DT (SEQ ID NO:138). Controls consisted of a negative control (no treatment); a preimmune adjuvant control (mice immunized with adjuvant only); and a positive control serum from mice immunized with peptide P10GTT (SEQ ID NO:237).

Peptide K13GTT consists of the sequence KREKTNFDPAEWG (SEQ ID NO:235) joined to the tetanus toxoid T-cell epitope to provide the sequence KREKTNFDPA EWGGPSLVDD ALINSTKIYS YFPSV (SEQ ID NO:236). The sequence KREKTNFDPA is an epitope recognized by autoantibodies from vasectomized men. K13G is also an epitope recognized by antibodies from monkeys immunized with human recombinant Sp17. These monkey antibodies recognize human sperm.

Peptide A9DT (SEQ ID NO:138) contains a nine amino acid sequence from the rabbit Sp17 sequence (AEWGAKVDD) coupled to a bovine RNAse T-cell epitope (T=NCAYKTTQANK) synthesized as part of the peptide.

Peptide P10GTT comprises the sequence PGGGTLPPSG, a peptide with known immunocontraceptive activity (*see* U.S. Patent No. 5,175,148 to O'Rand et al.) attached to the tetanus toxoid T-cell epitope (GPSLVDDALI NSTKIYSYFP SV) to provide a peptide of SEQ ID NO:237.

In oocytes receiving no treatment (negative control), 100% of oocytes were fertilized (n=28 oocytes). In oocytes treated with sera from mice immunized with

adjuvant only, 72% of oocytes were fertilized (n=11). In oocytes treated with sera from mice immunized with K13GTT, 33% of oocytes were fertilized (n=28). In oocytes treated with sera from mice immunized with recombinant whole Sp17, 29% of oocytes were fertilized (n=72). In oocytes treated with sera from mice immunized with peptide A9DT, 42% of oocytes were fertilized (n=72). In oocytes treated with sera from mice immunized with peptide P10GTT, 23% of oocytes were fertilized (n=74).

The above results indicate that immunization with peptide K13G, or with peptides containing the K13G epitope, would induce antibodies which would recognize human sperm. Such antibodies would be expected to inhibit fertilization, as antibodies to K13GTT and A9DT both inhibit fertilization in mouse oocytes. Antibodies to A9DT are recognized by human sperm.

EXAMPLE 18

Mimotope Analysis of Baboon Anti-human Sp17

Three female baboons were immunized with recombinant human Sp17 (SEQ ID NO:65). Each baboon received three injections; each injection contained 1 ml of water with 1 mg recombinant human Sp17, mixed with 1 ml of squalene:aracel A (4 squalene:aracel) (Sigma Co., St. Louis). Each injection was administered at four different sites, 1/2 ml per site, on day 0, then on days 21 and 35. Mimotope analysis was conducted using a human sequential decapeptide plate prepared as described in Example 13 above. Results are shown in **Figure 12**. Three peptides produced Z scores greater than two: KTNFDPAEWG (SEQ ID NO:20), AFRGHIAREE (SEQ ID NO:129) and GHIAREEAKK (SEQ ID NO:130).

EXAMPLE 19

Antibodies to hSp17 from Human Subjects

Sera obtained from human subjects known to contain anti-sperm antibody was assessed (clinically

tested using agglutination and immobilization tests) for immunoreactivity to human recombinant Sp17. Subjects 1-5 had been vasectomized (vx); subjects 6-7 had not been vasectomized; subject 9 was a male control (no anti-sperm antibodies); subject 10 was a female control (no anti-sperm antibodies).

Immunoreactivity of sera was assessed by ELISA as described in Example 2. Results are presented graphically in **Figure 13**. Each of the 8 patients known to possess anti-sperm antibodies were reactive to hSp17, compared to controls lacking known anti-sperm antibodies.

EXAMPLE 20

Mimotope Analysis of Serum from Infertile Human Patients

Mimotope analysis was conducted using a human sequential decapeptide plate prepared as described in Example 13 above, and using sera obtained from two human subjects with known infertility (defined as inability to impregnate partner within one year) and two fertile human subjects. Results are shown in **Figure 14A-14D**.

In infertile Patient 16A (**Figure 14a**), Z-scores greater than 2 were achieved using peptides KREKTNFDPA (SEQ ID NO:19), AVKIQAAFRG (SEQ ID NO:127) and IQAAFRGHIA (SEQ ID NO:128). In infertile Patient 8A (**Figure 14b**), Z-scores greater than 2 were seen with peptides AVKIQAAFRG (SEQ ID NO:127), IQAAFRGHIA (SEQ ID NO:128) and PFSNTHYRIP (SEQ ID NO:4); the Z-score of KREKTNFDPA (SEQ ID NO:19) was just less than 2. In the two fertile subjects tested, only peptides AVKIQAAFRG (SEQ ID NO:127) and IQAAFRGHIA (SEQ ID NO:128) provided Z-scores greater than 2 (**Figures 14c and 14d**).

EXAMPLE 21

Mimotope Analysis: Peptides of hSp17 Sequence (3 amino acid shifted)

The binding of immune sera from non-human primates to decapeptides of the human Sp17 sequence is summarized in **Table 1**, where (+) indicates a Z score of ≥ 1 and (++) indicates a Z score of ≥ 2. Production of decapeptides and mimotope analyses were carried out as described above. The decapeptides represent fragments of human Sp17; each subsequent decapeptide is shifted three amino acids along the Sp17 sequence. Sera was obtained from five non-human primates immunized with recombinant human Sp17 (SEQ ID NO:65). As can be seen in **Table 1**, certain decapeptides were associated with Z scores of ≥ 2.

TABLE 1

	NON-HUMAN PRIMATES				
MSIPFSNTHY-3	+		+		
PFSNTHYRIP-4					
NTHYRIPQGF-5					
YRIPQGFGNL-6					
PQGFGNLLEG-7					
FGNLLEGLTR-8					
LLEGLTREIL-9					
NIPAFAAAYF-14			+		
FESLLEKREK-105			++		
LLEKREKTNF-18					
KREKTNFDPA-19					
KTNFDPAEWG-20	++	++	++	++	++
FDPAEWGSKV-106	++	+		++	
AEWGSKVEDR-107	+			+	
GSKVEDRFYN-108	+	+	+		+
VEDRFYNNHA-109	+			+	++
RFYNNHAFEE-110	+				
NNHAFEEQEP-111	+			++	++
PPEKSDPKQE-114					+
KSDPKQEESQ-115					+
EVAAVKIQAA-126					
AVKIQAAFRG-127					
IQAAFRGHIA-128					
AFRGHIAREE-129		++	++	+	+
GHIAREEAKK-130		++	++	++	
AREEAKKMKT-131					
EAKKMKTNSL-132					
KMKTNSLQNE-133	+				

EXAMPLE 22

Reactivity of Human Sera to Recombinant HSp17

Sera samples obtained pre- and post-vasovasostomy from 15 men were analyzed for reactivity to recombinant HSp17 (rHSp17) using ELISA. Recombinant HSp17 (0.1μg/well) was used in ELISAs as described in Batova and O'Rand, *Biol. Reprod.* 54:1238 (1996). The plates were incubated for 2 hours in human sera (1:100 in PBST/2% milk) followed by a 1 hour incubation in horseradish peroxidase (HRP-conjugated goat anti-human IgA, IgG and IgM (1:1000 in PBST/2% milk) (Organon Teknika Corp., Durham NC). The reaction was developed as described previously (O'Rand and Widgren, *Reprod. Fertil. Devel.* 6:289 (1994). Control sera were from normal females and from vasectomized males and exhibited minimal reactivity to Sp17 (baseline anti-Sp17 reactivity). All sera were tested in quadruplicate and mean OD_{450nm} values calculated.

Of the 15 sera tested, 13 (87%) exhibited a statistically significant increase (Student's unpaired t test at the $P<0.05$ level) in anti-Sp17 reactivity when compared to control sera (**FIG. 17**). The level of antibody detected was variable in the majority of subjects (1,2,4,5,6,8,10,12,19 and 22) exhibiting low levels of anti-Sp17 reactivity ($OD_{450nm} \leq 0.2$ above control value) and three patients exhibiting more elevated levels of Sp17 antibodies (subjects 7, 11 and 16; $OD_{450nm} \geq 0.2$ above control value). No correlation was observed between the serum titre of antisperm antibodies and the level of anti-Sp17 reactivity (data not shown).

EXAMPLE 23

Reactivity of Human Sera to Recombinant HSp17

To determine the native HSp17 linear B cell epitopes that gave rise to the antibody response of **Figure 17A and B**, mimotope analyses of rHSp17 were

performed using the peptide pinblock method of Chiron Mimotopes as described in Example 14. Antisera reactivity was detected by ELISA (O'Rand and Widgren, 1994) using the primary antiserum at a dilution of 1:200 and the secondary antibody (HRP conjugated goat anti-human IgG, IgA and IgM) at a 1:5000 dilution. A pooled control serum taken from two non-vasectomized males with minimal reactivity to rHSp17 on ELISA was also tested on the same pin-block. The average control OD_{450nm} value was subsequently subtracted from the average immune value for each peptide. For each decapeptide a Z score was calculated; Z score = individual peptide pin reactivity - mean reactivity of all peptides/standard deviation for the antibody used (Pauls et al., *Mol. Immunol.* 30:709 (1993).

The overlapping decapeptides of HSp17 (7 amino acid overlap) were screened with sera from 13 patients taken pre and post vasovasostomy for the presence of antibody binding sites. The sera used exhibited a range of anti-Sp17 titres (**Fig. 17**) and were compared to a pool of control sera taken from non-vasectomized males with minimal reactivity to Sp17 on ELISA. Z-scores were calculated as described above, allowing the most antigenic regions of the molecule to be determined without comparisons of absolute OD_{450nm} values. **Figure 18** shows the results of a mimotope analysis and subsequent Z score determination using pre-vasovasostomy serum from subject 22. Immunodominant linear B cell epitopes were defined as peptide sequences to which antibody bound with a Z score $\geq$ 2. Subject 22 showed significant levels of antibody reactivity to two peptides at the N and C terminals of the molecule. The sequences of these peptides were PFSNTHYRIPQGFGNL (SEQ ID NO:238) and AVKIQAAFRG (SEQ ID NO:127).

Table 2 summarizes similar analyses using sera from 13 subjects. All subjects exhibited comparable patterns of antibody reactivity restricted predominantly

to two regions of the molecule. Subjects 1,2,4,5,7,8,10,11,12 and 22 each recognized epitopes within the peptide PFS-GNL (SEQ ID NO:238). Subjects 3, 6 and 16 had some reactivity to this peptide sequence but to a lesser extent. All sera reacted strongly to the sequence AVK-FRG (SEQ ID NO:127) except for serum from subject 1 where a lower level of binding was observed. A third less dominant epitope was also observed, KREKTNFDPA (SEQ ID NO:19) using sera from subjects 3 and 16. Antibody recognition of a fourth epitope (NIPAFAAAYF, SEQ ID NO:14) was shown in post-vasovasostomy serum from patient 1. Little qualitative difference was observed in the HSp17 linear B cell epitopes recognized by antibodies to native Sp17 before and after vasovasostomy (patients 1,5,7 and 11), although for each epitope some change in the relative amounts of antibody binding was seen.

The above results indicate that, while anti-Sp17 reactivity varied among subjects, the most predominant linear B cell epitopes were constant. The subjects' immunologic profiles varied in the number of epitopes recognized (less dominant epitopes recognized by fewer individuals) and the magnitude of response. However, despite a presumed outbred population, the most immunodominant epitopes ((SEQ ID NO:238 and SEQ ID NO:127) elicited a consistent response. Using antibodies raised to recombinant Sp17 and the linear peptide sequence K18C (Example 13, above), it has been shown that the C terminal B cell epitope of Sp17 (SEQ ID NO:70) is available to bind antibody on the principal piece of the tail during capacitation.

TABLE 2

Patient No.	1	1	2	3	4	5	5	6	7	7	8	10	11	11	12	16	22
**Pre/Post	A	B	B	A	A	A	B	B	A	B	A	B	A	B	A	A	A
MSIPFSNTHY-3		+															
PFSNTHYRIP-4	++	+	++	+	+	+	++	+	+		++	++		++	+	+	++
NTHYRIPQGF-5	++	+	++	+	+	+	++		++			++		++	++		++
YRIPQGFGNL-6	++	+	++	+	++	++	++		++	+		++	+	++	++		++
PQGFGNLLEG-7																	
FGNLLEGLTR-8			+							+						+	
LLEGLTREIL-9												+					
NIPAFAAAYF-14	+	++															
LLEKREKTNF-18		+				+											
KREKTNFDPA-19				++	+					+	+		+			++	
KTNFDPAEWG-20																	
EVAAVKIQAA-126		+				+							+				
AVKIQAAFRG-127	+	+	++	++	++	++	++	++	++	++	++	++	++	++	++	++	++
IQAAFRGHIA-128	+	+	+	++	+	+	+	++		++	++	++	++	+	++	++	+
AFRGHIAREE-129	+	+	+			+	+	+	+			+	+	+	+	+	+
GHIAREEAKK-130	+								+	+							
AREEAKKMKT-131	+				+	+	+	+	+	+							
EAKKMKTNSL-132	+	+			+	+	+	+		+		+				+	+

** Pre/Post: A indicates pre-vasovasostomy; B indicates post vasovasostomy.

EXAMPLE 24

Mimotope Analysis: Peptides of hSp17 Sequence (1 amino acid shift)

Tables 3 and 4 report the binding of immune sera from non-human primates, vasectomized male humans, and rabbits, to decapeptides of the human Sp17 sequence. Each decapeptide is shifted along the Sp17 sequence by one amino acid. In **Tables** 3 and 4, (+) indicates a Z score of $\geq$ 1 and (++) indicates a Z score of $\geq$ 2. Production of decapeptides and mimotope analyses were carried out as described above. Sera was obtained from four non-human primates immunized with recombinant human Sp17 (SEQ ID NO:65); from three vasectomized human males; and from two rabbits immunized with either recombinant human Sp17 (rabbit 9312) or human sperm (rabbit 7904).

Table 3 lists decapeptides, shifted by one amino acid, representing the human Sp17 amino acid sequence between amino acids 40 and 80 inclusive (*see* SEQ ID NO:2). **Table** 4 lists decapeptides, shifted by one amino acid, representing the human Sp17 amino acid sequence between amino acids 114-149 inclusive (*see* SEQ ID NO:2).

As can be seen in **Tables** 3 **and** 4, varied decapeptides were associated with Z scores of $\geq$ 2 in human, rabbit and non-human primate subjects.

TABLE 3

HSp17, RESIDUES 40-80 (1 AA SHIFT)

	NON-HUMAN PRIMATES				HUMANS			RABBITS	
	1271	1868	1811	Beethoven	16A I	8A I	3A F	9312	7904
AAYFESLLEK (104)									
AYFESLLEKR (165)						+		+	++
YFESLLEKRE (166)						+			
FESLLEKREK (105)									
ESLLEKREKT (167)									
SLLEKREKTN (168)									
LLEKREKTNF (18)									
LEKREKTNFD (169)									+
EKREKTNFDP (170)		+							
KREKTNFDPA (19)	++		+		+	+	+		
REKTNFDPAE (171)		+	+	++					
EKTNFDPAEW (172)									
KTNFDPAEWG (20)	+	++	++	++				+	
TNFDPAEWGS (173)									
NFDPAEWGSK (174)	+								
FDPAEWGSKV (106)									
DPAEWGSKVE (175)									
PAEWGSKVED (176)									
AEWGSKVEDR (107)				+					
EWGSKVEDRF (177)									
WGSKVEDRFY (178)		+	++					++	+
GSKVEDRFYN (108)	+	+	+					+	
SKVEDRFYNN (179)	+	+	+					+	
KVEDRFYNNH (180)	++	+	+	+				+	
VEDRFYNNHA (109)	+						++		
EDRFYNNHAF (181)									+

TABLE 3 (cont'd.)

HSp17, RESIDUES 40-80 (1 AA SHIFT)

DRFYNNHAFE (182)					++				++
RFYNNHAFEE (110)	+				+				
FYNNHAFEEQ (183)					++	+	+		
YNNHAFEEQE (184)							++		
NNHAFEEQEP (111)	+								
NHAFEEQEPP (185)									

TABLE 4

HSp17, RESIDUES 114-149 (1 AA SHIFT)

	NON-HUMAN PRIMATES				HUMANS			RABBITS	
	1271	1868	1811	Beethoven	16A I	8A I	3A F	9312	7904
EEVAAVKIQA (214)									
EVAAVKIQAA (126)									
VAAVKIQAAF (215)									
AAVKIQAAFR (216)					+		+		
AVKIQAAFRG (127)			+		++	+	++		
VKIQAAFRGH (217)			++		+	+	++		
KIQAAFRGHI (218)					++	+	++		
IQAAFRGHIA (128)								+	
QAAFRGHIAR (219)					++	++	++		
AAFRGHIARE (220)					+	+	+		
AFRGHIAREE (129)		++	+	+				++	
FRGHIAREEA (221)		+	+					++	++
RGHIAREEAK (222)		+	+		+	++			
GHIAREEAKK (130)	+	++	++	++					
HIAREEAKKM (223)		++	++	++					
IAREEAKKMK (224)				+					
AREEAKKMKT (131)									
REEAKKMKTN (225)									
EEAKKMKTNS (226)									
EAKKMKYNSL (132)									
AKKMKTNSLQ (227)	++		+		++	++	+		
KKMKTNSLQN (228)	++				++	++	+		
KMKTNSLQNE (133)	++			+					
MKTNSLQNEE (229)									+
KTNSLQNEEK (230)	+								

TABLE 4 (cont'd.)

IISp17, RESIDUES 114-149 (1 AA SHIFT)

TNSLQNEEKE (134)									
NSLQNEEKEE (231)									

EXAMPLE 25

Summary of Human Sp17 Sequences Containing Antigenic Epitopes

Table 5 provides a summary of human Sp17 fragments found by the present inventors to contain antigenic epitopes in mice, rabbit, non-human primates, and humans.

The foregoing examples are illustrative of the present invention, and are not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein.

TABLE 5

SUMMARY OF HSp17 SEQUENCES CONTAINING ANTIGENIC EPITOPES

	MICE	RABBITS	MONKEYS	HUMANS
MSIPFSNTHY (3)		X	X	X
SIPFSNTHYR (139)		X		X
IPFSNTHYRI (140)		X		X
PFSNTHYRIP (4)		X		X
FSNTHYRIPQ (141)				X
SNTHYRIPQG (142)				X
NTHYRIPQGF (5)				X
THYRIPQGFG (143)				X
HYRIPQGFGN (144)				X
YRIPQGFGNL (6)				X
RIPQGFGNLL (145)				X
IPQGFGNLLE (146)				X
PQGFGNLLEG (7)				X
QGFGNLLEGL (147)				X
GFGNLLEGLT (148)				X
FGNLLEGLTR (8)				X
GNLLEGLTRE (149)				X
NLLEGLTREI (150)				X
LLEGLTREIL (9)				X
LEGLTREILR (151)				
EGLTREILRE (152)				
GLTREILREQ (10)				
LTREILREQP (153)				
TREILREQPD (154)				
REILREQOPDN (11)				
EILREQPDNI (155)				
ILREQPDNIP (156)				
LREQPDNIPA (12)				
REQPDNIPAF (157)				
EQPDNIPAFA (158)				
QPDNIPAFAA (13)				
PDNIPAFAAA (159)				
DNIPAFAAAY (160)				
NIPAFAAAYF (14)	X	X	X	X
IPAFAAAYFE (161)				
PAFAAAYFES (162)				
AFAAAYFESL (103)				
FAAAYFESLL (163)				
AAAYFESLLE (164)				
AAYFESLLEK (104)				
AYFESLLEKR (165)		X		X
YFESLLEKRE (166)				X
FESLLEKREK (105)			X	X

	MICE	RABBITS	MONKEYS	HUMANS
ESLLEKREKT (167)			X	X
SLLEKREKTN (168)			X	X
LLEKREKTNF (18)			X	X
LEKREKTNFD (169)		X	X	X
EKREKTNFDP (170)		X	X	X
KREKTNFDPA (19)		X	X	X
REKTNFDPAE (171)		X	X	
EKTNFDPAEW (172)		X	X	
KTNFDPAEWG (20)		X	X	
TNFDPAEWGS (173)		X	X	
NFDPAEWGSK (174)		X	X	
FDPAEWGSKV (106)	X	X	X	
DPAEWGSKVE (175)	X	X	X	
PAEWGSKVED (176)		X	X	
AEWGSKVEDR (107)		X	X	
EWGSKVEDRF (177)		X	X	
WGSKVEDRFY (178)		X	X	
GSKVEDRFYN (108)		X	X	
SKVEDRFYNN (179)		X	X	
KVEDRFYNNH (180)		X	X	
VEDRFYNNHA (109)		X	X	X
EDRFYNNHAF (181)		X	X	X
DRFYNNHAFE (182)		X	X	X
RFYNNHAFEE (110)			X	X
FYNNHAFEEQ (183)			X	
YNNHAFEEQE (184)			X	
NNHAFEEQEP (111)			X	
NHAFEEQEPP (185)				
HAFEEQEPPE (186)				
AFEEQEPPEK (112)				
FEEQEPPEKS (187)				
EEQEPPEKSD (188)				
EQEPPEKSDP (113)				
QEPPEKSDPK (189)				
EPPEKSDPKQ (190)				
PPEKSDPKQE (114)			X	
PEKSDPKQEE (191)			X	
EKSDPKQEES (192)			X	
KSDPKQEESQ (115)			X	
SDPKQEESQI (193)				
DPKQEESQIS (194)				
PKQEESQISG (116)				
KQEESQISGK (195)				
QEESQISGKE (196)				
EESQISGKEE (117)				
ESQISGKEEE (197)				
SQISGKEEET (198)				

	MICE	RABBITS	MONKEYS	HUMANS
QISGKEEETS (118)				
ISGKEEETSV (199)				
SGKEEETSVT (200)				
GKEEETSVTI (119)				
KEEETSVTIL (201)				
EEETSVTILD (202)				
EETSVTILDS (120)				
ETSVTILDSS (203)				
TSVTILDSSE (204)				
SVTILDSSEE (121)				
VTILDSSEED (205)				
TILDSSEEDK (206)				
ILDSSEEDKE (122)				
LDSSEEDKEK (207)				
DSSEEDKEKE (208)				
SSEEDKEKEE (123)				
SEEDEKEEV (209)				
EEDKEKEEVA (210)				
EDKEKEEVAA (124)				
DKEKEEVAAV (211)				
KEKEEVAAVK (212)				
EKEEVAAVKI (125)				
KEEVAAVKIQ (213)				
EEVAAVKIQA (214)				
EVAAVKIQAA (126)				
VAAVKIQAAF (215)				
AAVKIQAAFR (216)				X
AVKIQAAFRG (127)		X	X	X
VKIQAAFRGH (217)		X	X	X
KIQAAFRGHI (218)		X	X	X
IQAAFRGHIA (128)	X	X	X	X
QAAFRGHIAR (219)	X	X	X	X
AAFRGHIARE (220)	X	X	X	X
AFRGHIAREE (129)	X	X	X	X
FRGHIAREEA (221)	X	X	X	X
RGHIAREEAK (222)	X	X	X	X
GHIAREEAKK (130)	X	X	X	X
HIAREEAKKM (223)		X	X	X
LAREEAKKMK (224)		X	X	X
AREEAKKMKT (131)		X	X	X
REEAKKMKTN (225)		X	X	X
EEAKKMKTNS (226)		X	X	X
EAKKMKYNSL (132)		X	X	X
AKKMKTNSLQ (227)		X	X	X
KKMKTNSLQN (228)		X	X	X
KMKTNSLQNE (133)		X	X	
MKTNSLQNEE (229)		X	X	

	MICE	RABBITS	MONKEYS	HUMANS
KTNSLQNEEK (230)			X	
TNSLQNEEKE (134)				
NSLQNEEKEE (231)				
SLQNEEKEEN (232)				
LQNEEKEENK (135)				

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: O'Rand, Michael G.
Widgren, Esther E.
Richardson, Richard T.
Lea, Isabel

(ii) TITLE OF INVENTION: Antigenic Sequences of a Sperm Protein and Immunocontraceptive Methods

(iii) NUMBER OF SEQUENCES: 239

(iv) CORRESPONDENCE ADDRESS:
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(B) STREET: P.O. Box 34009
(C) CITY: Charlotte
(D) STATE: North Carolina
(E) COUNTRY: USA
(F) ZIP: 28234

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Sibley, Kenneth D.
(B) REGISTRATION NUMBER: 31,665
(C) REFERENCE/DOCKET NUMBER: 5470-125

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 919-881-3140
(B) TELEFAX: 919-881-3175

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 854 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 32..484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GGAGGTTCCA TAGGCAGTTC TTACCAAGAA G ATG TCG ATT CCA TTC TCC AAC          52
                                   Met Ser Ile Pro Phe Ser Asn
                                     1               5

ACC CAC TAC CGA ATT CCA CAA GGA TTT GGG AAT CTT CTT GAA GGG CTG        100
Thr His Tyr Arg Ile Pro Gln Gly Phe Gly Asn Leu Leu Glu Gly Leu
        10                  15                  20

ACA CGC GAG ATT CTG AGA GAG CAA CCG GAC AAT ATA CCA GCT TTT GCA        148
Thr Arg Glu Ile Leu Arg Glu Gln Pro Asp Asn Ile Pro Ala Phe Ala
    25                  30                  35

GCA GCC TAT TTT GAG AGC CTT CTA GAG AAA AGA GAG AAA ACC AAC TTT        196
Ala Ala Tyr Phe Glu Ser Leu Leu Glu Lys Arg Glu Lys Thr Asn Phe
40                  45                  50                  55

GAT CCA GCA GAA TGG GGG AGT AAG GTA GAA GAC CGC TTC TAT AAC AAT        244
Asp Pro Ala Glu Trp Gly Ser Lys Val Glu Asp Arg Phe Tyr Asn Asn
                60                  65                  70

CAT GCA TTC GAG GAG CAA GAA CCA CCT GAG AAA AGT GAT CCT AAA CAA        292
His Ala Phe Glu Glu Gln Glu Pro Pro Glu Lys Ser Asp Pro Lys Gln
            75                  80                  85

GAA GAG TCT CAG ATA TCT GGG AAG GAG GAA GAG ACA TCA GTC ACC ATC        340
Glu Glu Ser Gln Ile Ser Gly Lys Glu Glu Glu Thr Ser Val Thr Ile
        90                  95                  100

TTA GAC TCT TCT GAG GAA GAT AAG GAA AAA GAA GAG GTT GCT GCT GTC        388
Leu Asp Ser Ser Glu Glu Asp Lys Glu Lys Glu Glu Val Ala Ala Val
    105                 110                 115

AAA ATC CAA GCT GCC TTC CGG GGA CAC ATA GCC AGA GAG GAG GCA AAG        436
Lys Ile Gln Ala Ala Phe Arg Gly His Ile Ala Arg Glu Glu Ala Lys
120                 125                 130                 135

AAA ATG AAA ACA AAT AGT CTT CAA AAT GAG GAA AAA GAG GAA AAC AAG        484
Lys Met Lys Thr Asn Ser Leu Gln Asn Glu Glu Lys Glu Glu Asn Lys
                140                 145                 150

TGAGGACACT GGTTTTACCT CCAGGAAACA TGAAAAATAA TCCAAATCCA TCCATCAACC      544

TTCTTATTAA TGTCATTTCT CCTTGAGGAA GGAAGATTTG ATGTTGTGAA ATAACATTCG      604

TTACTGTTGT GAAAATCTGT CATGAGCATT TGTTTAATAA GCATACCATT GAAACATGCC      664

ACTTGAAGAT TTCTCTGAGA TCATGAGTTT GTTTACACTT GTCTCAAGCC TATCTATAGA      724

GACCCTTGGA TTTAGAATTA TAGAACTAAA GTATCTGAGA TTACAGAGAT CTCAGAGGTT      784

ATGTGTTCTA ACTATTATCA AATGAATAAA TCCTCTCTAT CACATCCCCC AAAAAAAAAA      844

AAAAAAAAAA                                                             854
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ile Pro Phe Ser Asn Thr His Tyr Arg Ile Pro Gln Gly Phe
1 5 10 15

Gly Asn Leu Leu Glu Gly Leu Thr Arg Glu Ile Leu Arg Glu Gln Pro
20 25 30

Asp Asn Ile Pro Ala Phe Ala Ala Ala Tyr Phe Glu Ser Leu Leu Glu
35 40 45

Lys Arg Glu Lys Thr Asn Phe Asp Pro Ala Glu Trp Gly Ser Lys Val
50 55 60

Glu Asp Arg Phe Tyr Asn Asn His Ala Phe Glu Glu Gln Glu Pro Pro
65 70 75 80

Glu Lys Ser Asp Pro Lys Gln Glu Glu Ser Gln Ile Ser Gly Lys Glu
85 90 95

Glu Glu Thr Ser Val Thr Ile Leu Asp Ser Ser Glu Glu Asp Lys Glu
100 105 110

Lys Glu Glu Val Ala Ala Val Lys Ile Gln Ala Ala Phe Arg Gly His
115 120 125

Ile Ala Arg Glu Glu Ala Lys Lys Met Lys Thr Asn Ser Leu Gln Asn
130 135 140

Glu Glu Lys Glu Glu Asn Lys
145 150

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Ile Pro Phe Ser Asn Thr His Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro Phe Ser Asn Thr His Tyr Arg Ile Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn Thr His Tyr Arg Ile Pro Gln Gly Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr Arg Ile Pro Gln Gly Phe Gly Asn Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Gln Gly Phe Gly Asn Leu Leu Glu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Phe Gly Asn Leu Leu Glu Gly Leu Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Leu Glu Gly Leu Thr Arg Glu Ile Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Leu Thr Arg Glu Ile Leu Arg Glu Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg Glu Ile Leu Arg Glu Gln Pro Asp Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Arg Glu Gln Pro Asp Asn Ile Pro Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gln Pro Asp Asn Ile Pro Ala Phe Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Ile Pro Ala Phe Ala Ala Ala Tyr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Phe Ala Ala Ala Tyr Phe Glu Asn Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Ala Tyr Phe Glu Asn Leu Leu Glu Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe Glu Asn Leu Leu Glu Lys Arg Glu Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Leu Glu Lys Arg Glu Lys Thr Asn Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Lys Arg Glu Lys Thr Asn Phe Asp Pro Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys Thr Asn Phe Asp Pro Ala Glu Trp Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Phe Asp Pro Ala Glu Trp Gly Ala Lys Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ala Glu Trp Gly Ala Lys Val Asp Asp Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gly Ala Lys Val Asp Asp Arg Phe Tyr Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Val Asp Asp Arg Phe Tyr Asn Asn His Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Arg Phe Tyr Asn Asn His Ala Phe Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Asn Asn His Ala Phe Gln Glu His Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ala Phe Gln Glu His Glu Ser Glu Lys Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Glu His Glu Ser Glu Lys Cys Glu Ala Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ser Glu Lys Cys Glu Ala Glu Glu Lys Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Cys Glu Ala Glu Glu Lys Ser Gln Ser Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Glu Lys Ser Gln Ser Val Thr Glu Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ser Gln Ser Val Thr Glu Glu Glu Thr Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Thr Glu Glu Glu Thr Pro Val Leu Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu Glu Thr Pro Val Leu Thr Ile Asp Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Pro Val Leu Thr Ile Asp Ser Glu Asp Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Thr Ile Asp Ser Glu Asp Asp Lys Asp Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ser Glu Asp Asp Lys Asp Lys Glu Glu Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp Lys Asp Lys Glu Glu Met Ala Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Lys Glu Glu Met Ala Ala Leu Lys Ile Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Ala Ala Leu Lys Ile Gln Ala Ala Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Leu Lys Ile Gln Ala Ala Phe Arg Gly His
1 5 10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gln Ala Ala Phe Arg Gly His Leu Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Phe Arg Gly His Leu Ala Arg Glu Asp Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

His Leu Ala Arg Glu Asp Val Lys Lys Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Arg Glu Asp Val Lys Lys Ile Arg Thr Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Val Lys Lys Ile Arg Thr Asn Lys Ala Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ile Arg Thr Asn Lys Ala Glu Glu Glu Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Asn Lys Ala Glu Glu Glu Thr Glu Glu Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Lys Ala Glu Glu Glu Thr Glu Glu Asn Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Ser Ile Pro Phe Ser Asn Thr His Tyr Arg Ile Pro Gln Gly Phe
1 5 10 15

Gly Asn Leu Leu Glu Gly Leu Thr Arg Glu Ile Leu Arg Glu Gln Pro
20 25 30

Asp Asn Ile Pro Ala Phe Ala Ala Ala Tyr Phe Glu Asn Leu Leu Glu
35 40 45

Lys Arg Glu Lys Thr Asn Phe Asp Pro Ala Glu Trp Gly Ala Lys Val

50 55 60

Asp Asp Arg Phe Tyr Asn Asn His Ala Phe Gln Glu His Glu Ser Glu
65 70 75 80

Lys Cys Glu Ala Glu Glu Lys Ser Gln Ser Val Thr Glu Glu Glu Thr
85 90 95

Pro Val Leu Thr Ile Asp Ser Glu Asp Asp Lys Asp Lys Glu Glu Met
100 105 110

Ala Ala Leu Lys Ile Gln Ala Ala Phe Arg Gly His Ile Ala Arg Glu
115 120 125

Asp Val Lys Lys Ile Arg Thr Asn Lys Ala Glu Glu Glu Thr Glu Glu
130 135 140

Asn Asn
145

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Ser Ile Pro Phe Ser Asn Thr His Tyr Arg Ile Pro Gln Gly Phe
1 5 10 15

Gly Asn Leu Leu Glu Gly Leu Thr Arg Glu Ile Leu Arg Glu Gln Pro
20 25 30

Asp Asn Ile Pro Ala Phe Ala Ala Ala Tyr Phe Glu Asn Leu Leu Glu
35 40 45

Lys Arg Glu Lys Thr Ser Phe Asp Pro Ala Glu Trp Gly Ala Lys Val
50 55 60

Glu Asp Arg Phe Tyr Asn Asn His Ala Phe Lys Glu Gln Glu Gln Val
65 70 75 80

Glu Lys Cys Glu Gln Glu Leu Ala Lys Ser Ser Gly Arg Glu Glu Thr
85 90 95

Pro Val Thr Pro Phe Glu Glu Ser Thr Glu Glu Glu Arg Glu Gln Glu
100 105 110

Glu Ala Ala Ala Leu Lys Ile Gln Ser Leu Phe Arg Gly His Val Ala

115 120 125

Arg Glu Glu Val Lys Lys Met Lys Ser Asp Lys Asn Glu Asn Leu Lys
130 135 140

Glu Glu Ala Asp Asn
145

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Pro Phe Ser Asn Thr His Tyr Arg Ile Pro Gln Gly Phe Gly Asn Leu
1 5 10 15

Leu Glu Gly Leu Thr Arg Glu Ile Leu
20 25

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Asn Ile Pro Ala Phe Ala Ala Ala Tyr Phe Glu Asn Leu Leu Glu Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asn Ile Pro Ala Phe Ala Ala Ala Tyr Phe Glu Ser Leu Leu Glu Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Phe Asp Pro Ala Glu Trp Gly Ala Lys Val Asp Asp Arg Phe Tyr Asn
1 5 10 15

Asn His Ala Phe Gln Glu His Glu Ser Glu Lys Cys
20 25

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Phe Asp Pro Ala Glu Trp Gly Ala Lys Val Glu Asp Arg Phe Tyr Asn
1 5 10 15

Asn His Ala Phe Lys Glu Gln Glu Gln Val Glu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Phe Asp Pro Ala Glu Trp Gly Ser Lys Val Glu Asp Arg Phe Tyr Asn
1 5 10 15

Asn His Ala Phe Glu Glu Gln Glu Pro Pro Glu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Ala Ala Leu Lys Ile Gln Ala Ala Phe Arg Gly His Ile Ala Arg
1 5 10 15

Glu Asp Val Lys Lys
20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Ala Ala Leu Lys Ile Gln Ser Leu Phe Arg Gly His Val Ala Arg
1 5 10 15

Glu Glu Val Lys Lys
20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Val Ala Ala Val Lys Ile Gln Ala Ala Phe Arg Gly His Ile Ala Arg
1 5 10 15

Glu Glu Ala Lys Lys
20

(2) INFORMATION FOR SEQ ID NO:61

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gly Ala Lys Val Asp Asp Arg Phe Tyr Asn Asn His Ala Phe Gln Glu
1 5 10 15

His Glu Ser Glu Lys Cys
20

(2) INFORMATION FOR SEQ ID NO:62

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCGGATCCA TGTCGATTCC ATTTTCC 27

(2) INFORMATION FOR SEQ ID NO:63

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

CGGGGTACCG CCAGTGCCCT CAATTGT 27

(2) INFORMATION FOR SEQ ID NO:64

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Arg Gly Ser His His His His His His Gly Ser Ile Pro Gln Gly Phe
1 5 10 15

Gly Asn Leu Leu Glu Gly Leu Thr Arg Glu Ile Leu Arg Glu Gln Pro
20 25 30

Asp Asn Ile Pro Ala Phe Ala Ala Ala Tyr Phe Glu Asn Leu Leu Glu
35 40 45

Lys Arg Glu Lys Thr Asn Phe Asp Pro Ala Glu Trp Gly Ala Lys Val
50 55 60

Asp Asp Arg Phe Tyr Asn Asn His Ala Phe Gln Glu His Glu Ser Glu
65 70 75 80

Lys Cys Glu Ala Glu Glu Lys Ser Gln Ser Val Thr Glu Glu Glu Thr
85 90 95

Pro Val Leu Thr Ile Asp Ser Glu Asp Asp Lys Asp Lys Glu Glu Met
100 105 110

Ala Ala Leu Lys Ile Gln Ala Ala Phe Arg Gly His Ile Ala Arg Glu
115 120 125

Asp Val Lys Lys Ile Arg Thr Asn Lys Ala Glu Glu Glu Thr Glu Glu
130 135 140

Asn Asn
145

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Arg Gly Ser His His His His His Gly Ser Met Ser Ile Pro Phe
1 5 10 15

Ser Asn Thr His Tyr Arg Ile Pro Gln Gly Phe Gly Asn Leu Leu Glu
20 25 30

Gly Leu Thr Arg Glu Ile Leu Arg Glu Gln Pro Asp Asn Ile Pro Ala
35 40 45

Phe Ala Ala Ala Tyr Phe Glu Ser Leu Leu Glu Lys Arg Glu Lys Thr
50 55 60

Asn Phe Asp Pro Ala Glu Trp Gly Ser Lys Val Glu Asp Arg Phe Tyr
65 70 75 80

Asn Asn His Ala Phe Glu Glu Gln Glu Pro Pro Glu Lys Ser Asp Pro
85 90 95

Lys Gln Glu Glu Ser Gln Ile Ser Gly Lys Glu Glu Glu Thr Ser Val
100 105 110

Thr Ile Leu Asp Ser Ser Glu Glu Asp Lys Glu Lys Glu Glu Val Ala
115 120 125

Ala Val Lys Ile Gln Ala Ala Phe Arg Gly His Ile Ala Arg Glu Glu
130 135 140

Ala Lys Lys Met Lys Thr Asn Ser Leu Gln Asn Glu Glu Lys Glu Glu
145 150 155 160

Asn Lys

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 895 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 80..568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

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AGCAACGAGA AAAACAACCG GAACCGGCGG CACCTGCTTG GAGAGAAAGG AGGTTCCATA      60

GGCAGTTCTT ACCAAGAAG ATG TCG ATT CCA TTC TCC AAC ACC CAC TAC CGA      112
                     Met Ser Ile Pro Phe Ser Asn Thr His Tyr Arg
                       1               5                  10

ATT CCA CAA GGA TTT GGG AAT CTT CTT GAA GGG CTG ACA CGC GAG ATT      160
Ile Pro Gln Gly Phe Gly Asn Leu Leu Glu Gly Leu Thr Arg Glu Ile
            15                  20                  25

CTG AGA GAG CAA CCG GAC AAT ATA CCA GCT TTT GCA GCC TAT TTT GAG      208
Leu Arg Glu Gln Pro Asp Asn Ile Pro Ala Phe Ala Ala Tyr Phe Glu
        30                  35                  40

AGC CTT CTA GAG AAA AGA GAG AAA ACC AAC TTT GAT CCA GCA GAA TGG      256
Ser Leu Leu Glu Lys Arg Glu Lys Thr Asn Phe Asp Pro Ala Glu Trp
    45                  50                  55

GGG AGT AAG GTA GAA GAC CGC TTC TAT AAC AAC AAT CAT GCA TTC GAG      304
Gly Ser Lys Val Glu Asp Arg Phe Tyr Asn Asn Asn His Ala Phe Glu
60                  65                  70                  75

GAG CAA GAA CCA CCT GAG AAA AGT GAT CCT AAA CAA GAA GAA TCT CAG      352
Glu Gln Glu Pro Pro Glu Lys Ser Asp Pro Lys Gln Glu Glu Ser Gln
                80                  85                  90

GTA TCT GGG AAG GAG GAA GAG ACA TCA GTC ACC ATC TTA GAC TCT TCT      400
Val Ser Gly Lys Glu Glu Glu Thr Ser Val Thr Ile Leu Asp Ser Ser
            95                  100                 105

GAG GAA GAT AAG GAA AAA GAA GAG GTT GCT GCT GTC AAA ATC CAA GCT      448
Glu Glu Asp Lys Glu Lys Glu Glu Val Ala Ala Val Lys Ile Gln Ala
        110                 115                 120

GCC TTC CGG GGA CAC GTA GCC AGA GAG GAG GTA AAG AAA ATG AAA ACA      496
Ala Phe Arg Gly His Val Ala Arg Glu Glu Val Lys Lys Met Lys Thr
    125                 130                 135

GAT AGT CTT CAA AAT GAG GAA AAA GAG GAA AAC AGT GAG GAC ACT GGT      544
Asp Ser Leu Gln Asn Glu Glu Lys Glu Glu Asn Ser Glu Asp Thr Gly
140                 145                 150                 155

TTT ACC TCC AGG ACA CAT GAA AAA TAATCCAAAT CCATCAACCT TCTTGTTAAT      598
Phe Thr Ser Arg Thr His Glu Lys
                160

GTCATTTTTT CCTGAGGAAG GAAGATTTGA TGTTGTGAAA TAACATTCGT TGCTGTTGTG      658
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AAAATCCGTC ATGAGCATTT GTTTAATAAG CATACCATTG AAACATGCCA CTTGAAGATT 718

TCTCTGAGAT CATGAGTTTG TTTACACTTG TCTCAAGCCT ATCTATAGAG ACCCTTGGAT 778

TTAGAATTAC AGAACAAAAG TATCTGAGAT TACAGAGATC TCAGAGGTTA TGTGTTTTAA 838

CCATTATCAA ATGAATAAAT CCTCTCTATC ACATCCCAAA AAAAAAAAAA AAAAAAA 895

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Ser Ile Pro Phe Ser Asn Thr His Tyr Arg Ile Pro Gln Gly Phe
1 5 10 15

Gly Asn Leu Leu Glu Gly Leu Thr Arg Glu Ile Leu Arg Glu Gln Pro
20 25 30

Asp Asn Ile Pro Ala Phe Ala Ala Tyr Phe Glu Ser Leu Leu Glu Lys
35 40 45

Arg Glu Lys Thr Asn Phe Asp Pro Ala Glu Trp Gly Ser Lys Val Glu
50 55 60

Asp Arg Phe Tyr Asn Asn Asn His Ala Phe Glu Glu Gln Glu Pro Pro
65 70 75 80

Glu Lys Ser Asp Pro Lys Gln Glu Glu Ser Gln Val Ser Gly Lys Glu
85 90 95

Glu Glu Thr Ser Val Thr Ile Leu Asp Ser Ser Glu Glu Asp Lys Glu
100 105 110

Lys Glu Glu Val Ala Ala Val Lys Ile Gln Ala Ala Phe Arg Gly His
115 120 125

Val Ala Arg Glu Glu Val Lys Lys Met Lys Thr Asp Ser Leu Gln Asn
130 135 140

Glu Glu Lys Glu Glu Asn Ser Glu Asp Thr Gly Phe Thr Ser Arg Thr
145 150 155 160

His Glu Lys

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Arg Ile Pro Gln Gly Phe Gly Asn Leu Leu Glu Gly Leu Thr Arg Glu
1 5 10 15

Ile Leu Arg Glu Gln
20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Ser Lys Val Glu Asp Arg Phe Tyr Asn Asn His Ala Phe Glu Glu Gln
1 5 10 15

Glu Pro Pro Glu Lys
20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Lys Ile Gln Ala Ala Phe Arg Gly His Ile Ala Arg Glu Glu Ala
5 10 15

Lys Lys

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Leu Leu Glu Lys Arg Glu Lys Thr Ser Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Lys Arg Glu Lys Thr Ser Phe Asp Pro Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Lys Thr Ser Phe Asp Pro Ala Glu Trp Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:
Ala Glu Trp Gly Ala Lys Val Glu Asp Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Gly Ala Lys Val Glu Asp Arg Phe Tyr Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Val Glu Asp Arg Phe Tyr Asn Asn His Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Arg Phe Tyr Asn Asn His Ala Phe Lys Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asn Asn His Ala Phe Lys Glu Gln Glu Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ala Phe Lys Glu Gln Glu Gln Val Glu Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Glu Gln Glu Gln Val Glu Lys Cys Glu Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gln Val Glu Lys Cys Glu Gln Glu Leu Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Lys Cys Glu Gln Glu Leu Ala Lys Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Gln Glu Leu Ala Lys Ser Ser Gly Arg Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Ala Lys Ser Ser Gly Arg Glu Glu Thr Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Ser Gly Arg Glu Glu Thr Pro Val Thr Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Glu Glu Thr Pro Val Thr Pro Phe Glu Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Pro Val Thr Pro Phe Glu Glu Ser Thr Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Pro Phe Glu Glu Ser Thr Glu Glu Glu Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Glu Ser Thr Glu Glu Glu Arg Glu Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Glu Glu Glu Arg Glu Gln Glu Glu Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Arg Glu Gln Glu Glu Ala Ala Ala Leu Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Glu Glu Ala Ala Ala Leu Lys Ile Gln Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Ala Ala Leu Lys Ile Gln Ser Leu Phe Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Lys Ile Gln Ser Leu Phe Arg Gly His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Ser Leu Phe Arg Gly His Val Ala Arg Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Arg Gly His Val Ala Arg Glu Glu Val Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Val Ala Arg Glu Glu Val Lys Lys Met Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Glu Glu Val Lys Lys Met Lys Ser Asp Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Lys Lys Met Lys Ser Asp Lys Asn Glu Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Lys Ser Asp Lys Asn Glu Asn Leu Lys Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Lys Asn Glu Asn Leu Lys Glu Glu Ala Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Asn Glu Asn Leu Lys Glu Glu Ala Asp Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Ala Phe Ala Ala Ala Tyr Phe Glu Ser Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Ala Ala Tyr Phe Glu Ser Leu Leu Glu Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Phe Glu Ser Leu Leu Glu Lys Arg Glu Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Phe Asp Pro Ala Glu Trp Gly Ser Lys Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Ala Glu Trp Gly Ser Lys Val Glu Asp Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Gly Ser Lys Val Glu Asp Arg Phe Tyr Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Val Glu Asp Arg Phe Tyr Asn Asn His Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Arg Phe Tyr Asn Asn His Ala Phe Glu Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Asn Asn His Ala Phe Glu Glu Gln Glu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ala Phe Glu Glu Gln Glu Pro Pro Glu Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Glu Gln Glu Pro Pro Glu Lys Ser Asp Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Pro Pro Glu Lys Ser Asp Pro Lys Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Lys Ser Asp Pro Lys Gln Glu Glu Ser Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Pro Lys Gln Glu Glu Ser Gln Ile Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Glu Glu Ser Gln Ile Ser Gly Lys Glu Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Gln Ile Ser Gly Lys Glu Glu Glu Thr Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Gly Lys Glu Glu Glu Thr Ser Val Thr Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Glu Glu Thr Ser Val Thr Ile Leu Asp Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ser Val Thr Ile Leu Asp Ser Ser Glu Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ile Leu Asp Ser Ser Glu Glu Asp Lys Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Ser Ser Glu Glu Asp Lys Glu Lys Glu Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Glu Asp Lys Glu Lys Glu Glu Val Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Glu Lys Glu Glu Val Ala Ala Val Lys Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Glu Val Ala Ala Val Lys Ile Gln Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ala Val Lys Ile Gln Ala Ala Phe Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Ile Gln Ala Ala Phe Arg Gly His Ile Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Ala Phe Arg Gly His Ile Ala Arg Glu Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Gly His Ile Ala Arg Glu Glu Ala Lys Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ala Arg Glu Glu Ala Lys Lys Met Lys Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Glu Ala Lys Lys Met Lys Thr Asn Ser Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Lys Met Lys Thr Asn Ser Leu Gln Asn Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Thr Asn Ser Leu Gln Asn Glu Glu Lys Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Leu Gln Asn Glu Glu Lys Glu Glu Asn Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Gly Gly Gly Thr Leu Pro Pro Ser Gly Asn Cys Ala Tyr Lys Thr Thr
5 10 15

Gln Ala Asn Lys
20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Val Asp Asp Arg Phe Tyr Asn Asn His Asn Cys Ala Tyr Lys Thr Thr
5 10 15

Gln Ala Asn Lys
20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Asn Cys Ala Tyr Lys Thr Thr Gln Ala Asn Lys Ala Glu Trp Gly Ala
5 10 15

Lys Val Glu Asp
20

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Ser Ile Pro Phe Ser Asn Thr His Tyr Arg
5 10

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ile Pro Phe Ser Asn Thr His Tyr Arg Ile
5 10

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Phe Ser Asn Thr His Tyr Arg Ile Pro Gln
5 10

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Ser Asn Thr His Tyr Arg Ile Pro Gln Gly
5 10

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Thr His Tyr Arg Ile Pro Gln Gly Phe Gly
5 10

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

His Tyr Arg Ile Pro Gln Gly Phe Gly Asn
5 10

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Arg Ile Pro Gln Gly Phe Gly Asn Leu Leu
5 10

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Ile Pro Gln Gly Phe Gly Asn Leu Leu Glu
5 10

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Gln Gly Phe Gly Asn Leu Leu Glu Gly Leu
5 10

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Gly Phe Gly Asn Leu Leu Glu Gly Leu Thr
5 10

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Gly Asn Leu Leu Glu Gly Leu Thr Arg Glu
5 10

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Asn Leu Leu Glu Gly Leu Thr Arg Glu Ile
5 10

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Leu Glu Gly Leu Thr Arg Glu Ile Leu Arg
5 10

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Glu Gly Leu Thr Arg Glu Ile Leu Arg Glu
5 10

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Leu Thr Arg Glu Ile Leu Arg Glu Gln Pro
5 10

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Thr Arg Glu Ile Leu Arg Glu Gln Pro Asp
5 10

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Glu Ile Leu Arg Glu Gln Pro Asp Asn Ile
5 10

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Ile Leu Arg Glu Gln Pro Asp Asn Ile Pro
5 10

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Arg Glu Gln Pro Asp Asn Ile Pro Ala Phe
5 10

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Glu Gln Pro Asp Asn Ile Pro Ala Phe Ala
5 10

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Pro Asp Asn Ile Pro Ala Phe Ala Ala Ala
5 10

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Asp Asn Ile Pro Ala Phe Ala Ala Ala Tyr
5 10

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Ile Pro Ala Phe Ala Ala Ala Tyr Phe Glu
5 10

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Pro Ala Phe Ala Ala Ala Tyr Phe Glu Ser
5 10

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Phe Ala Ala Ala Tyr Phe Glu Ser Leu Leu
5 10

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ala Ala Ala Tyr Phe Glu Ser Leu Leu Glu
5 10

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Ala Tyr Phe Glu Ser Leu Leu Glu Lys Arg
5 10

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Tyr Phe Glu Ser Leu Leu Glu Lys Arg Glu
5 10

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Glu Ser Leu Leu Glu Lys Arg Glu Lys Thr
5 10

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Ser Leu Leu Glu Lys Arg Glu Lys Thr Asn
5 10

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Leu Glu Lys Arg Glu Lys Thr Asn Phe Asp
5 10

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Glu Lys Arg Glu Lys Thr Asn Phe Asp Pro
5 10

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Arg Glu Lys Thr Asn Phe Asp Pro Ala Glu
5 10

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Glu Lys Thr Asn Phe Asp Pro Ala Glu Trp
5 10

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Thr Asn Phe Asp Pro Ala Glu Trp Gly Ser
5 10

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Asn Phe Asp Pro Ala Glu Trp Gly Ser Lys
5 10

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Asp Pro Ala Glu Trp Gly Ser Lys Val Glu
5 10

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Pro Ala Glu Trp Gly Ser Lys Val Glu Asp
5 10

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Glu Trp Gly Ser Lys Val Glu Asp Arg Phe
5 10

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Trp Gly Ser Lys Val Glu Asp Arg Phe Tyr
5 10

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Ser Lys Val Glu Asp Arg Phe Tyr Asn Asn
5 10

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Lys Val Glu Asp Arg Phe Tyr Asn Asn His
5 10

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Glu Asp Arg Phe Tyr Asn Asn His Ala Phe
5 10

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Asp Arg Phe Tyr Asn Asn His Ala Phe Glu
5 10

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Phe Tyr Asn Asn His Ala Phe Glu Glu Gln
5 10

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Tyr Asn Asn His Ala Phe Glu Glu Gln Glu
5 10

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Asn His Ala Phe Glu Glu Gln Glu Pro Pro
5 10

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

His Ala Phe Glu Glu Gln Glu Pro Pro Glu
5 10

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Phe Glu Glu Gln Glu Pro Pro Glu Lys Ser
5 10

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Glu Glu Gln Glu Pro Pro Glu Lys Ser Asp
5 10

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Gln Glu Pro Pro Glu Lys Ser Asp Pro Lys
5 10

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Glu Pro Pro Glu Lys Ser Asp Pro Lys Gln
5 10

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Pro Glu Lys Ser Asp Pro Lys Gln Glu Glu
5 10

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Glu Lys Ser Asp Pro Lys Gln Glu Glu Ser
5 10

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Ser Asp Pro Lys Gln Glu Glu Ser Gln Ile
5 10

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Asp Pro Lys Gln Glu Glu Ser Gln Ile Ser
5 10

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Lys Gln Glu Glu Ser Gln Ile Ser Gly Lys
5 10

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Gln Glu Glu Ser Gln Ile Ser Gly Lys Glu
5 10

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Glu Ser Gln Ile Ser Gly Lys Glu Glu Glu
5 10

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Ser Gln Ile Ser Gly Lys Glu Glu Glu Thr
5 10

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Ile Ser Gly Lys Glu Glu Glu Thr Ser Val
5 10

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Ser Gly Lys Glu Glu Glu Thr Ser Val Thr
5 10

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Lys Glu Glu Glu Thr Ser Val Thr Ile Leu
5 10

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Glu Glu Glu Thr Ser Val Thr Ile Leu Asp
5 10

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Glu Thr Ser Val Thr Ile Leu Asp Ser Ser
5 10

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Thr Ser Val Thr Ile Leu Asp Ser Ser Glu
5 10

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Val Thr Ile Leu Asp Ser Ser Glu Glu Asp
5 10

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Thr Ile Leu Asp Ser Ser Glu Glu Asp Lys
5 10

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Leu Asp Ser Ser Glu Glu Asp Lys Glu Lys
5 10

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Asp Ser Ser Glu Glu Asp Lys Glu Lys Glu
5 10

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Ser Glu Glu Asp Lys Glu Lys Glu Glu Val
5 10

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Glu Glu Asp Lys Glu Lys Glu Glu Val Ala
5 10

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Asp Lys Glu Lys Glu Glu Val Ala Ala Val
5 10

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Lys Glu Lys Glu Glu Val Ala Ala Val Lys
5 10

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Lys Glu Glu Val Ala Ala Val Lys Ile Gln
5 10

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Glu Glu Val Ala Ala Val Lys Ile Gln Ala
5 10

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Val Ala Ala Val Lys Ile Gln Ala Ala Phe
5 10

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Ala Ala Val Lys Ile Gln Ala Ala Phe Arg
5 10

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Val Lys Ile Gln Ala Ala Phe Arg Gly His
5 10

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Lys Ile Gln Ala Ala Phe Arg Gly His Ile
5 10

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Gln Ala Ala Phe Arg Gly His Ile Ala Arg
5 10

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Ala Ala Phe Arg Gly His Ile Ala Arg Glu
5 10

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Phe Arg Gly His Ile Ala Arg Glu Glu Ala
5 10

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Arg Gly His Ile Ala Arg Glu Glu Ala Lys
5 10

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

His Ile Ala Arg Glu Glu Ala Lys Lys Met
5 10

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Ile Ala Arg Glu Glu Ala Lys Lys Met Lys
5 10

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Arg Glu Glu Ala Lys Lys Met Lys Thr Asn
5 10

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Glu Glu Ala Lys Lys Met Lys Thr Asn Ser
5 10

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Ala Lys Lys Met Lys Thr Asn Ser Leu Gln
5 10

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Lys Lys Met Lys Thr Asn Ser Leu Gln Asn
5 10

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Met Lys Thr Asn Ser Leu Gln Asn Glu Glu
5 10

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Lys Thr Asn Ser Leu Gln Asn Glu Glu Lys
5 10

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Asn Ser Leu Gln Asn Glu Glu Lys Glu Glu
5 10

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Ser Leu Gln Asn Glu Glu Lys Glu Glu Asn
5 10

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Lys Arg Glu Lys Thr Asn Phe Asp Pro Ala Glu Trp Gly Ser Lys Val
5 10 15

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234

Ala Val Lys Ile Gln Ala Ala Phe Arg Gly His Ile Ala Arg Glu Glu
5 10 15

Ala Lys Lys

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235

Lys Arg Glu Lys Thr Asn Phe Asp Pro Ala Glu Trp Gly
5 10

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

Lys Arg Glu Lys Thr Asn Phe Asp Pro Ala Glu Trp Gly Gly Pro Ser
5 10 15

Leu Val Asp Asp Ala Leu Ile Asn Ser Thr Lys Ile Tyr Ser Tyr Phe
20 25 30

Pro Ser Val
35

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

Pro Gly Gly Gly Thr Leu Pro Pro Ser Gly Gly Pro Ser Leu Val Asp
5 10 15

Asp Ala Leu Ile Asn Ser Thr Lys Ile Tyr Ser Tyr Phe Pro Ser Val
20 25 30

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

Pro Phe Ser Asn Thr His Tyr Arg Ile Pro Gln Gly Phe Gly Asn Leu
5 10 15

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Lys Ile Gln Ala Ala Phe Arg Gly His Ile Ala Arg Glu Glu Ala
5 10 15

Lys Lys Cys

THAT WHICH IS CLAIMED IS:

1. An peptide selected from the group consisting of:

(a) antigenic peptides having an amino acid sequence selected from the group consisting of SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:128, SEQ ID NO:233, and SEQ ID NO:234; and

(b) fragments of the antigenic peptides of (a) which are at least six amino acids in length.

2. An immunocontraceptive method, comprising administering to a subject a peptide according to claim 1 in an amount effective to reduce the fertility of said subject.

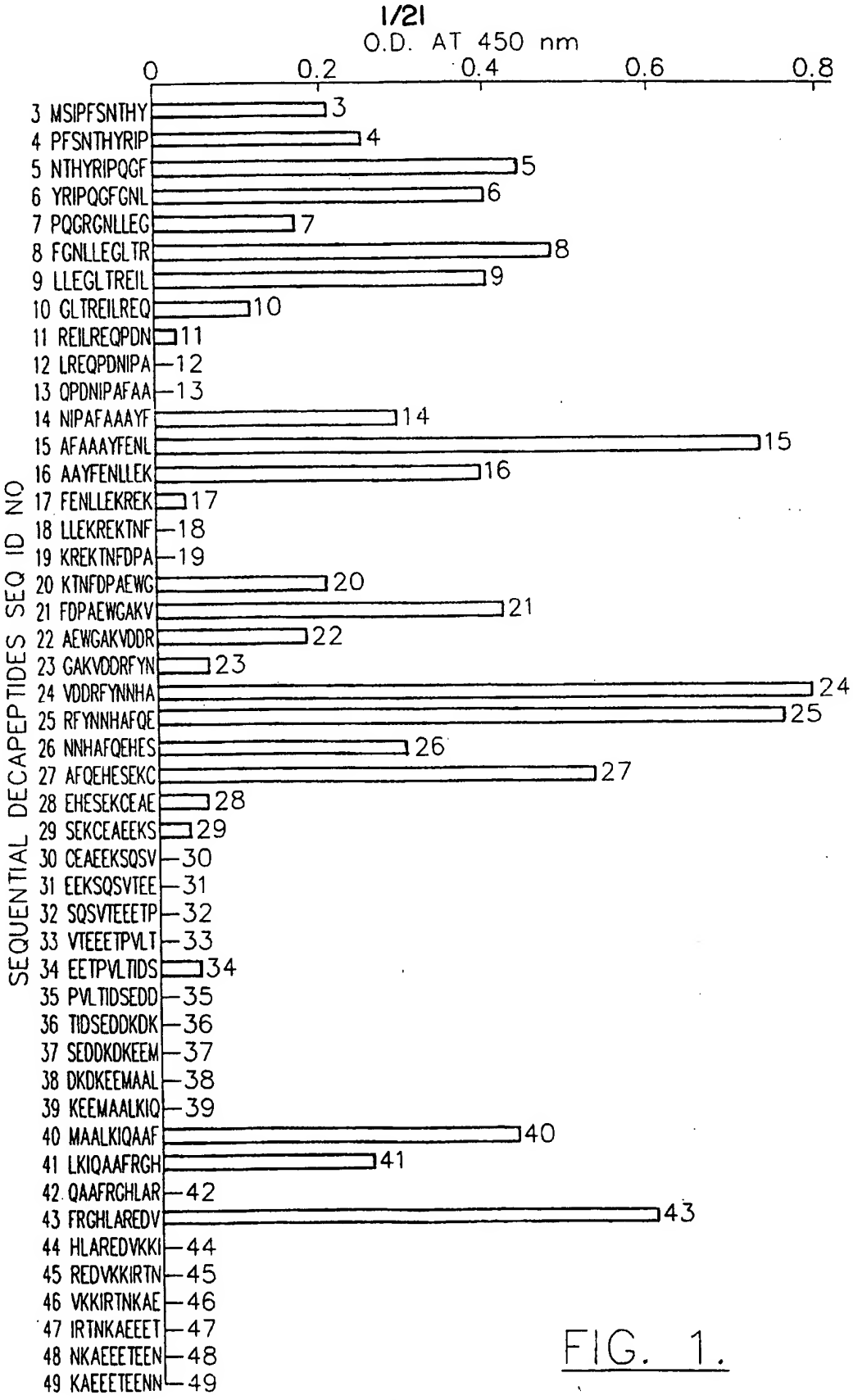
3. An immunocontraceptive method according to claim 2, wherein said subject is a female subject.

4. An immunocontraceptive method, comprising administering to a subject a combination of at least two peptides according to claim 1 in an amount effective to reduce the fertility of said subject.

5. An immunocontraceptive method according to claim 4, wherein said subject is a female subject.

6. An immunocontraceptive vaccine formulation comprising a peptide according to claim 1 in an amount effective to reduce the fertility of a subject in combination with a pharmaceutically acceptable carrier.

7. An immunocontraceptive vaccine formulation comprising a combination of peptides according to claim 4, in an amount effective to reduce the fertility of said subject in combination with a pharmaceutically acceptable carrier.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0.2
0.4
0.6
0.8
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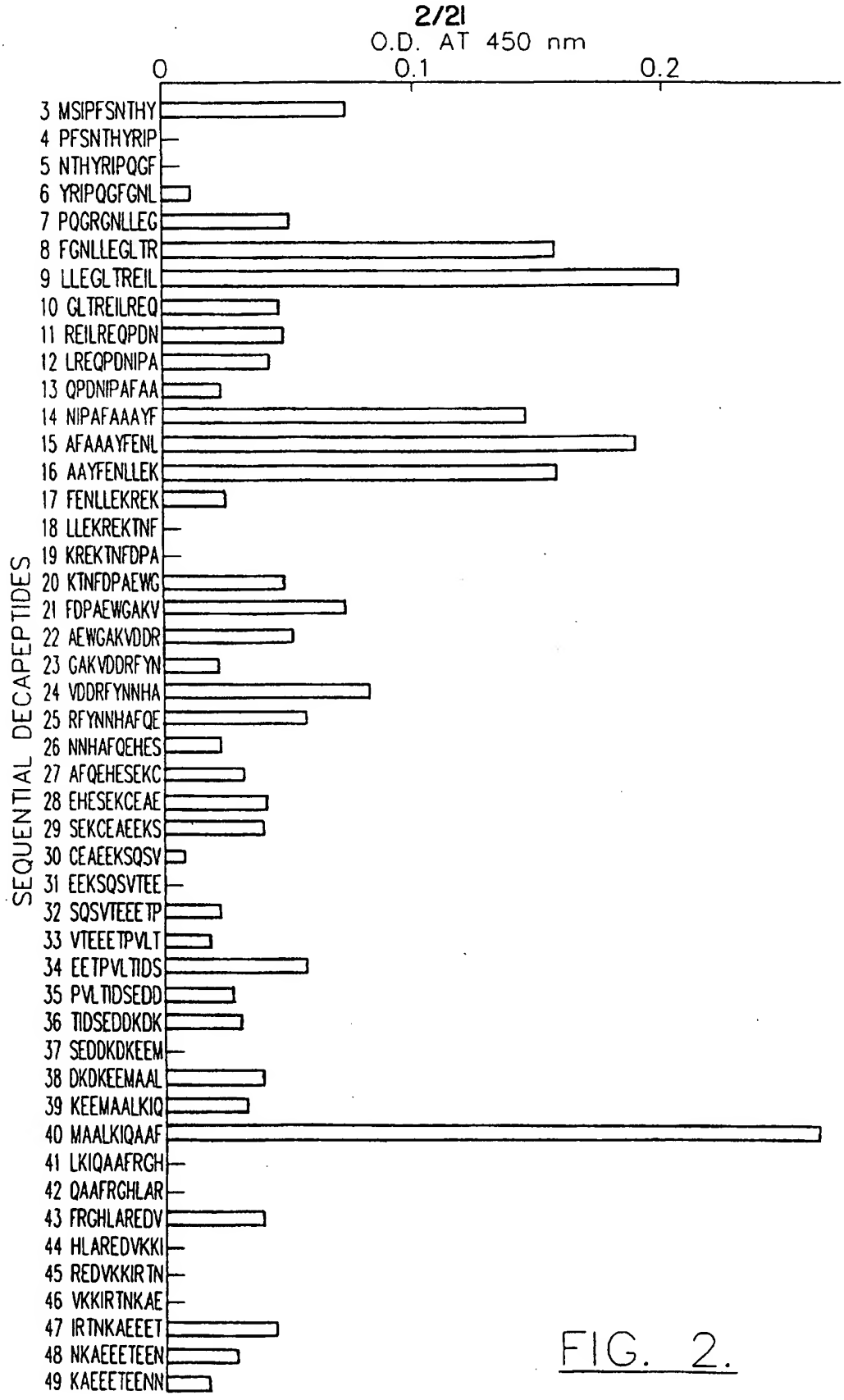
4 PFSNTHYRIP 4
5 NTHYRIPQGF 5
6 YRIPQGFGNL 6
7 PQGRGNLLEG 7
8 FGNLLEGLTR 8
9 LLEGLTREIL 9
10 GLTREILREQ 10
11 REILREQPDN 11
12 LREQPDNIPA 12
13 QPDNIPAFAA 13
14 NIPAFAAAYF 14
15 AFAAAYFENL 15
16 AAYFENLLEK 16
17 FENLLEKREK 17
18 LLEKREKTNF 18
19 KREKTNFDPA 19
20 KTNFDPAEWG 20
21 FDPAEWGAKV 21
22 AEWGAKVDDR 22
23 GAKVDDRFYN 23
24 VDDRFYNNHA 24
25 RFYNNHAFQE 25
26 NNHAFQEHES 26
27 AFQEHESEKC 27
28 EHESEKCEAE 28
29 SEKCEAEEKS 29
30 CEAEEKSQSV 30
31 EEKSQSVTEE 31
32 SQSVTEEETP 32
33 VTEEETPVLT 33
34 EETPVLTIDS 34
35 PVLTIDSEDD 35
36 TIDSEDDKDK 36
37 SEDDKDKEEM 37
38 DKDKEEMAAL 38
39 KEEMAALKIQ 39
40 MAALKIQAAF 40
41 LKIQAAFRGH 41
42 QAAFRGHLAR 42
43 FRGHLAREDV 43
44 HLAREDVKKI 44
45 REDVKKIRTN 45
46 VKKIRTNKAE 46
47 IRTNKAEEET 47
48 NKAEEETEEN 48
49 KAEEETEENN 49

FIG. 1.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8 FGNLLEGLTR
9 LLEGLTREIL
10 GLTREILREQ
11 REILREQPDN
12 LREQPDNIPA
13 QPDNIPAFAA
14 NIPAFAAAYF
15 AFAAAYFENL
16 AAYFENLLEK
17 FENLLEKREK
18 LLEKREKTNF
19 KREKTNFDPA
20 KTNFDPAEWG
21 FDPAEWGAKV
22 AEWGAKVDDR
23 GAKVDDRFYN
24 VDDRFYNNHA
25 RFYNNHAFQE
26 NNHAFQEHES
27 AFQEHESEKC
28 EHESEKCEAE
29 SEKCEAEEKS
30 CEAEEKSQSV
31 EEKSQSVTEE
32 SQSVTEEETP
33 VTEEETPVLT
34 EETPVLTIDS
35 PVLTIDSEDD
36 TIDSEDDKDK
37 SEDDKDKEEM
38 DKDKEEMAAL
39 KEEMAALKIQ
40 MAALKIQAAF
41 LKIQAAFRGH
42 QAAFRGHLAR
43 FRGHLAREDV
44 HLAREDVKKI
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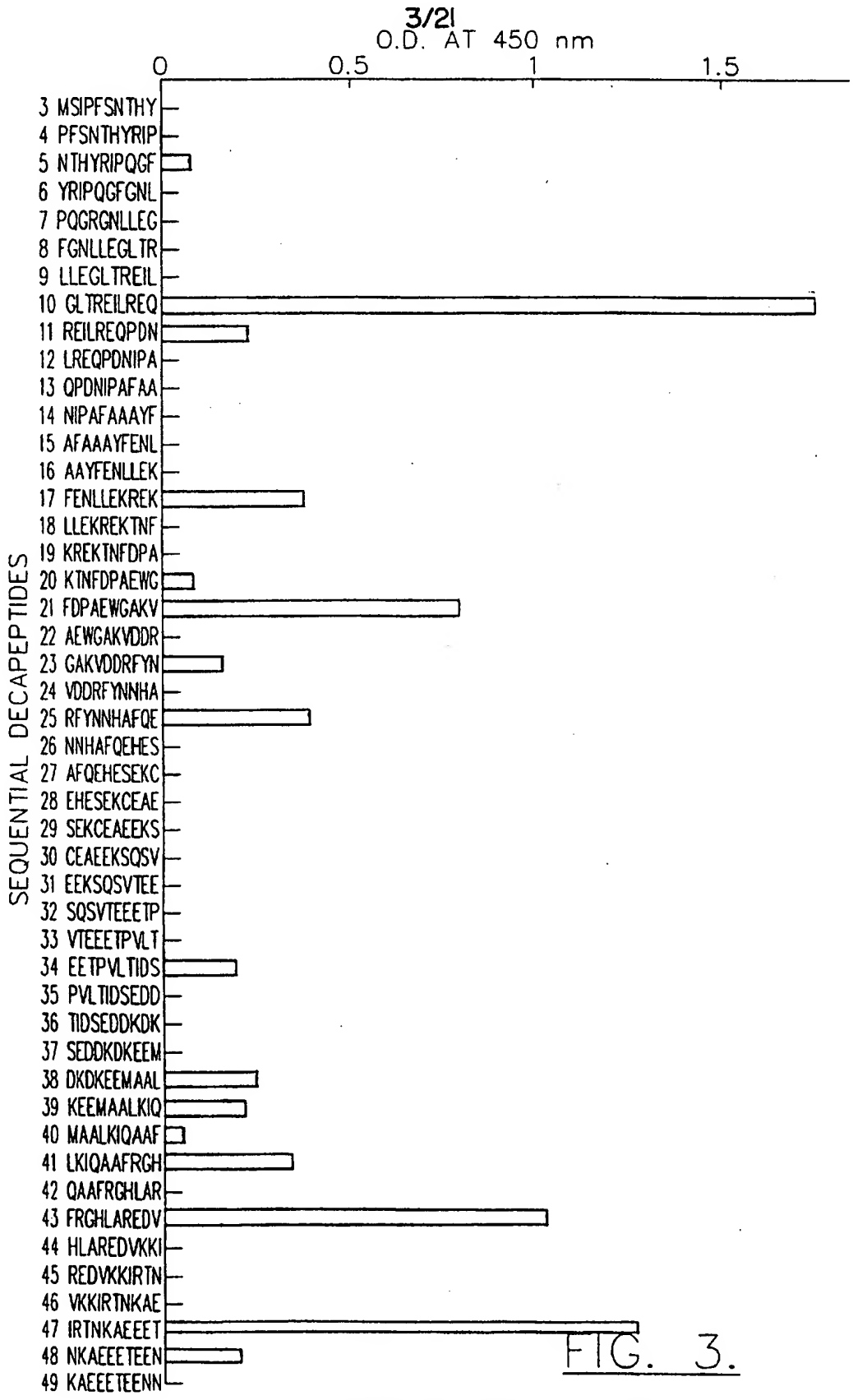
46 VKKIRTNKAE
47 IRTNKAEEET
48 NKAEEETEEN
49 KAEEETEENN

FIG. 2.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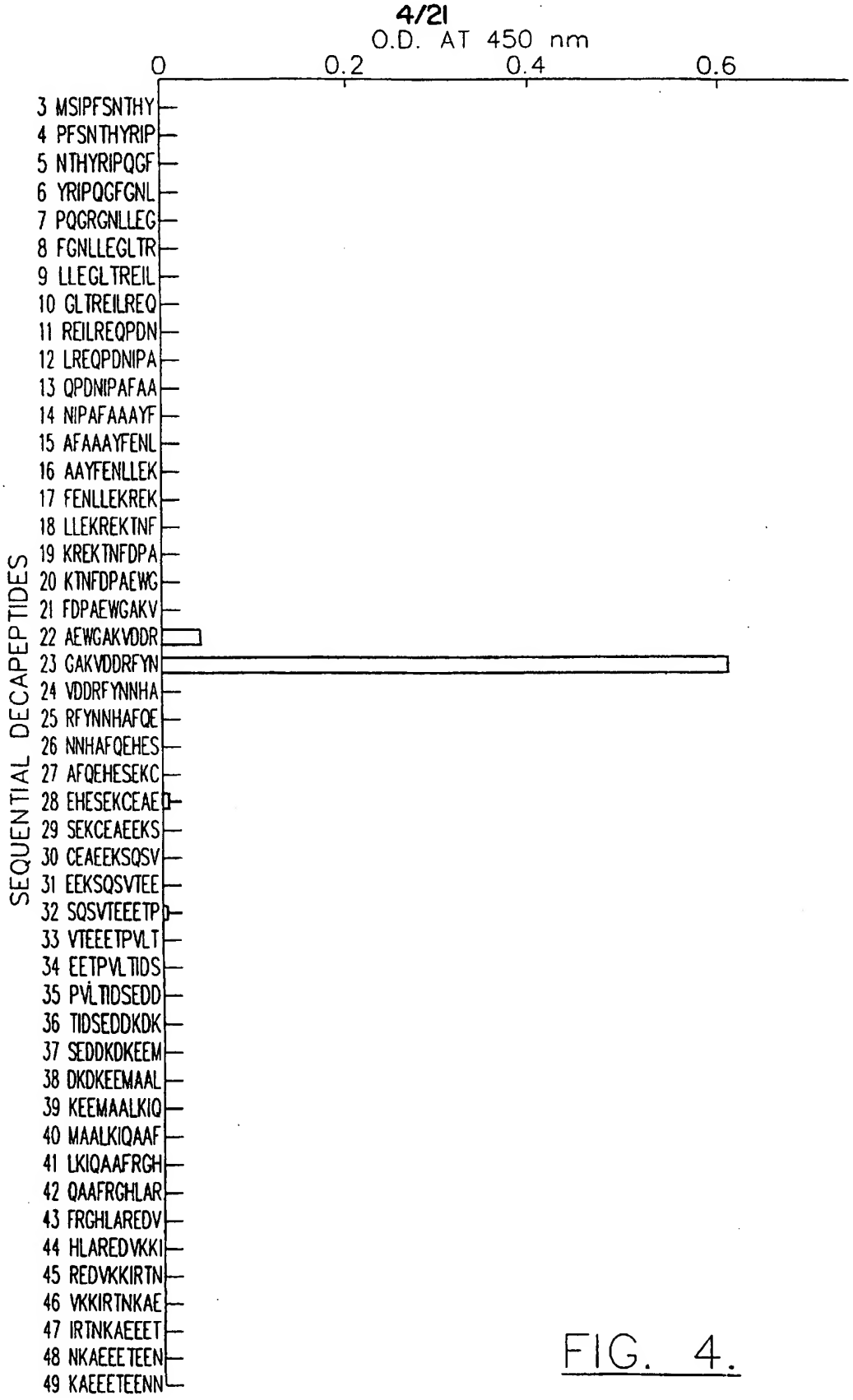
6 YRIPQGFGNL
7 PQGRGNLLEG
8 FGNLLEGLTR
9 LLEGLTREIL
10 GLTREILREQ
11 REILREQPDN
12 LREQPDNIPA
13 QPDNIPAFAA
14 NIPAFAAAYF
15 AFAAAYFENL
16 AAYFENLLEK
17 FENLLEKREK
18 LLEKREKTNF
19 KREKTNFDPA
20 KTNFDPAEWG
21 FDPAEWGAKV
22 AEWGAKVDDR
23 GAKVDDRFYN
24 VDDRFYNNHA
25 RFYNNHAFQE
26 NNHAFQEHES
27 AFQEHESEKC
28 EHESEKCEAE
29 SEKCEAEEKS
30 CEAEEKSQSV
31 EEKSQSVTEE
32 SQSVTEEETP
33 VTEEETPVLT
34 EETPVLTIDS
35 PVLTIDSEDD
36 TIDSEDDKDK
37 SEDDKDKEEM
38 DKDKEEMAAL
39 KEEMAALKIQ
40 MAALKIQAAF
41 LKIQAAFRGH
42 QAAFRGHLAR
43 FRGHLAREDV
44 HLAREDVKKI
45 REDVKKIRTN
46 VKKIRTNKAE
47 IRTNKAEEET
48 NKAEEETEEN
49 KAEEETEENN

FIG. 3.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0.4
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6 YRIPQGFGNL
7 PQGRGNLLEG
8 FGNLLEGLTR
9 LLEGLTREIL
10 GLTREILREQ
11 REILREQPDN
12 LREQPDNIPA
13 QPDNIPAFAA
14 NIPAFAAAYF
15 AFAAAYFENL
16 AAYFENLLEK
17 FENLLEKREK
18 LLEKREKTNF
19 KREKTNFDPA
20 KTNFDPAEWG
21 FDPAEWGAKV
22 AEWGAKVDDR
23 GAKVDDRFYN
24 VDDRFYNNHA
25 RFYNNHAFQE
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27 AFQEHESEKC
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29 SEKCEAEEKS
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32 SQSVTEEETP
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38 DKDKEEMAAL
39 KEEMAALKIQ
40 MAALKIQAAF
41 LKIQAAFRGH
42 QAAFRGHLAR
43 FRGHLAREDV
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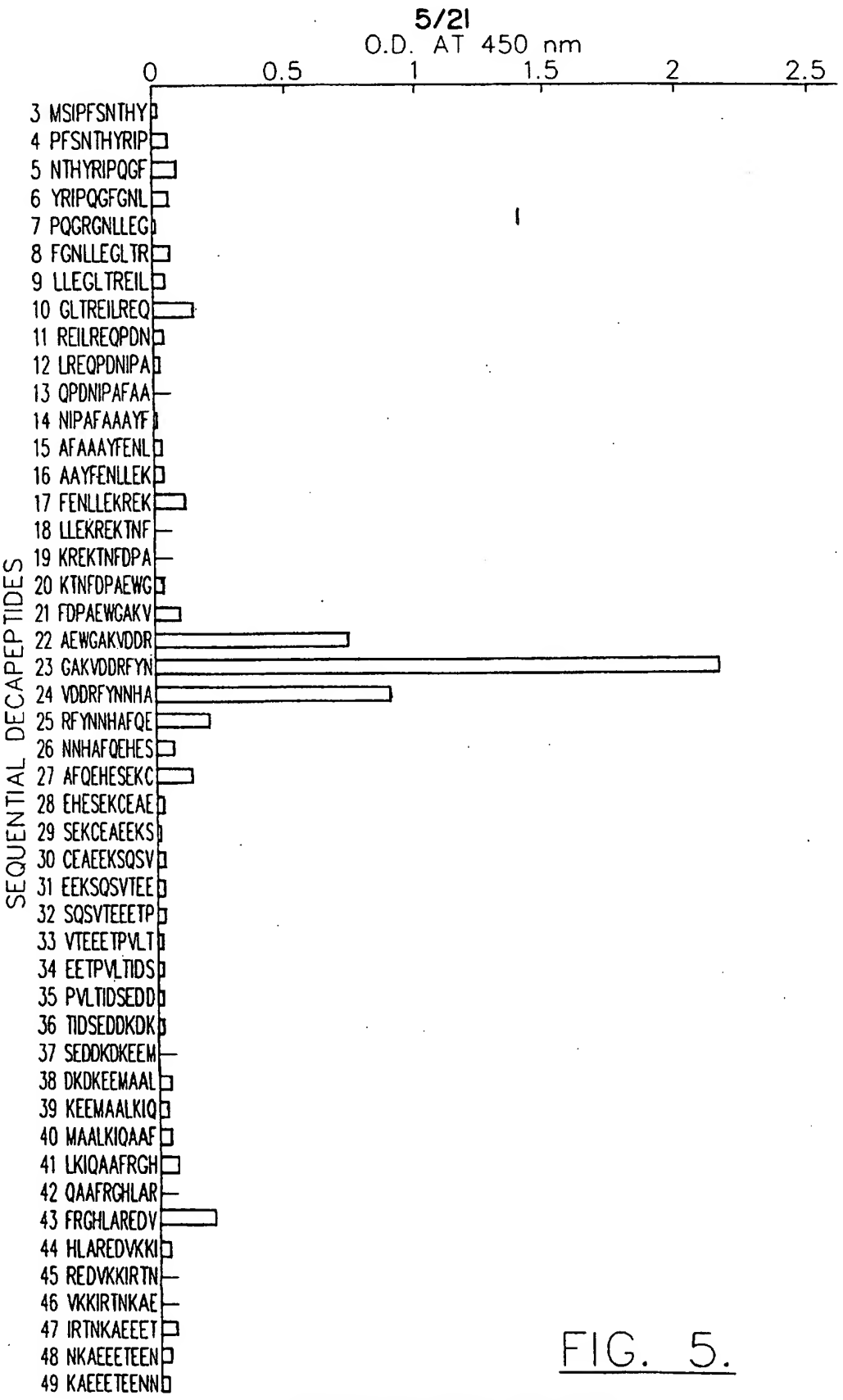
48 NKAEEETEEN
49 KAEEETEENN

FIG. 4.


5/21
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8 FGNLLEGLTR
9 LLEGLTREIL
10 GLTREILREQ
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12 LREQPDNIPA
13 QPDNIPAFAA
14 NIPAFAAAYF
15 AFAAAYFENL
16 AAYFENLLEK
17 FENLLEKREK
18 LLEKREKTNF
19 KREKTNFDPA
20 KTNFDPAEWG
21 FDPAEWGAKV
22 AEWGAKVDDR
23 GAKVDDRFYN
24 VDDRFYNNHA
25 RFYNNHAFQE
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35 PVLTIDSEDD
36 TIDSEDDKDK
37 SEDDKDKEEM
38 DKDKEEMAAL
39 KEEMAALKIQ
40 MAALKIQAAF
41 LKIQAAFRGH
42 QAAFRGHLAR
43 FRGHLAREDV
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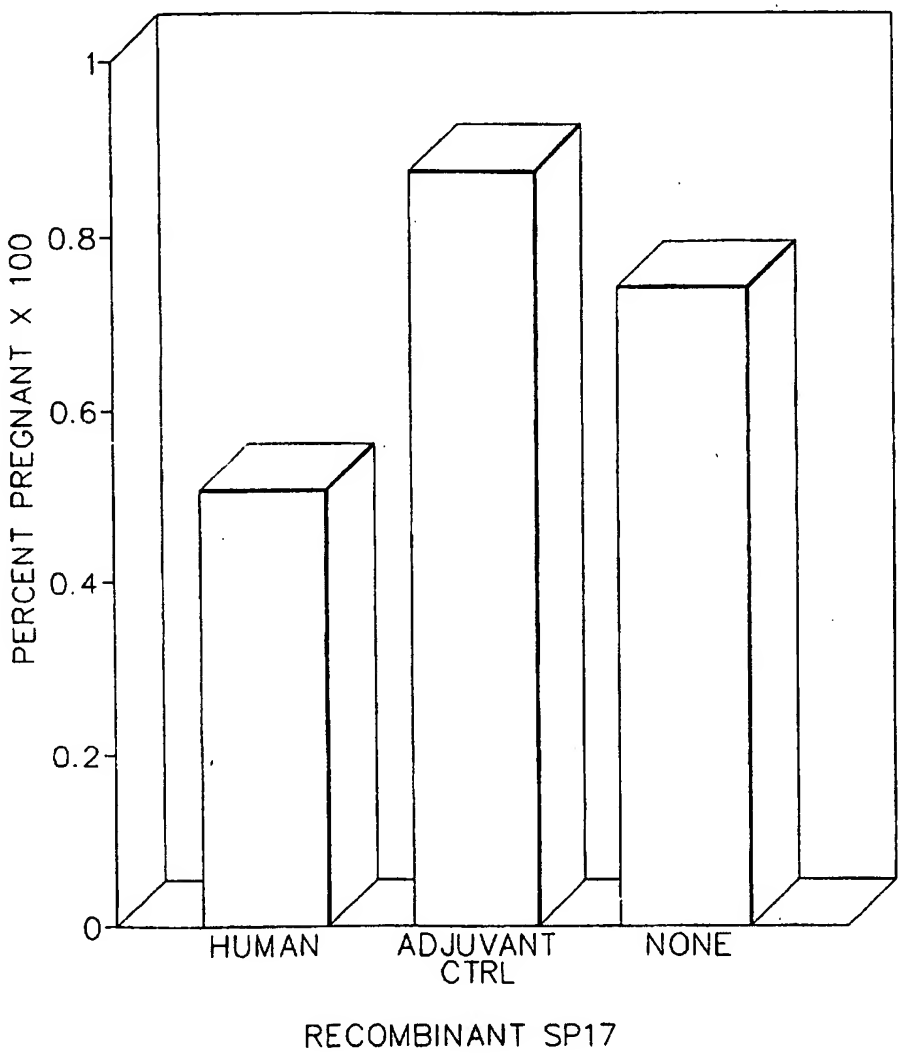
48 NKAEEETEEN
49 KAEEETEENN

FIG. 5.


PERCENT PREGNANT X 100
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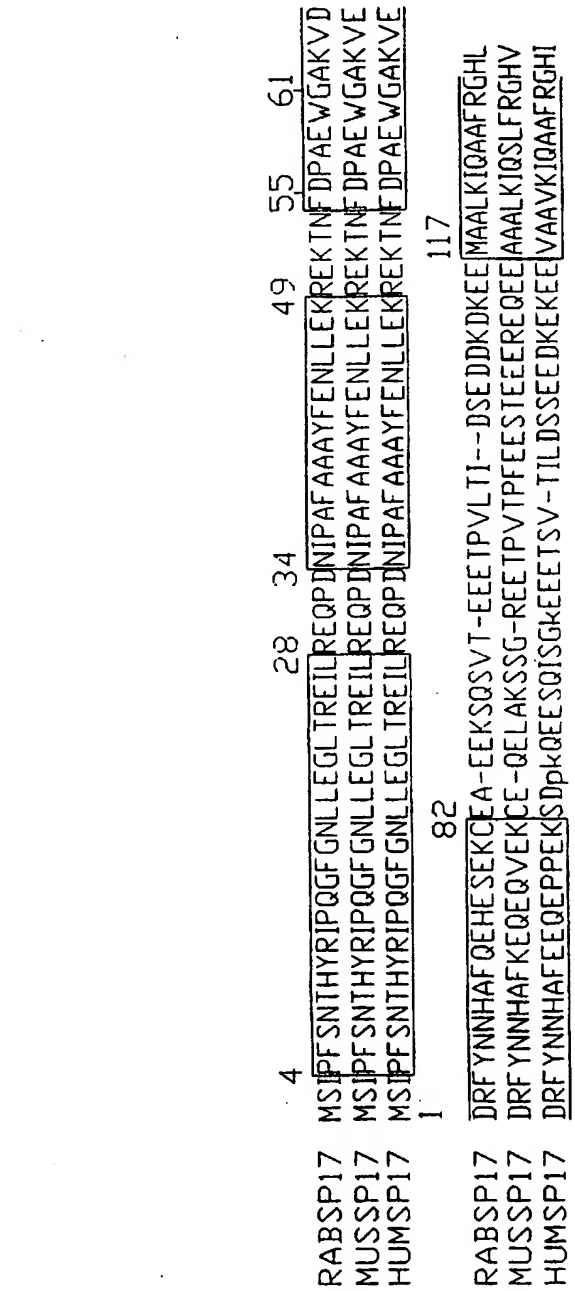
0.4
0.2
0
HUMAN
ADJUVANT CTRL
NONE
RECOMBINANT SP17

FIG. 6.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HUMSP17 MSIPFSNTHYRIPQGFGNLLEGLTREILREQPDNIPAFAAAYFENLLEKREKTNFDPAEWGAKVE
1 82 117
RABSP17 DRFYNNHAFQEHESEKCEA-EEKSQSVT-EEETPVLTI--DSEDDKDKEEMAALKIQAAFRGHL
MUSSP17 DRFYNNHAFKEQEQVEKCE-QELAKSSG-REETPVTPFEESTEEEREQEEAAALKIQSLFRGHV
HUMSP17 DRFYNNHAFEEQEPPEKSDpkQEESQISGkEEETSV-TILDSSEEDKEKEEVAAVKIQAAFRGHI
137
RABSP17 AREDVKKIRTNKAEEETEENN-
MUSSP17 AREEVKKMKSDKNENLKEEADn
HUMSP17 AREEAKKMKTNSLQNEEKEENk
151

FIG. 7.

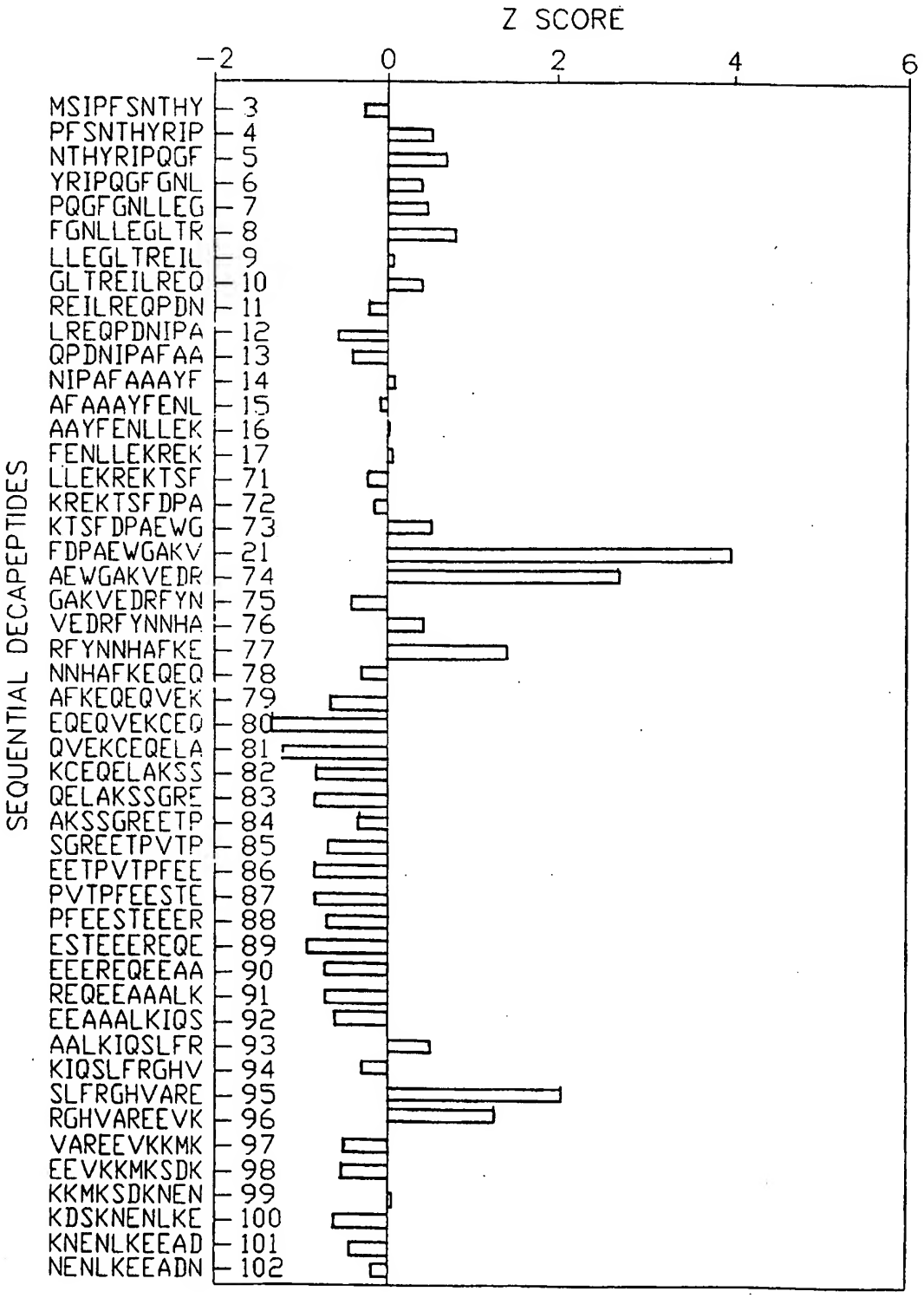
```
          1                                                  50
babsp17   MSIPFSNTHY RIPQGFGNLL EGLTREILRE QPDNIPAFAA AYFESLLEKR
humsp17   MSIPFSNTHY RIPQGRGNLL EGLTREILRE QPDNIPAFAA AYFESLLEKR
rabsp17   MSIPFSNTHY RIPQGFGNLL EGLTREILRE QPDNIPAFAA AYFENLLEKR
mussp17   MSIPFSNTHY RIPQGFGNLL EGLTREILRE QPDNIPAFAA AYFENLLEKR

          51                                                 100
babsp17   EKTNFDPAEW GSKVEDRFYN NHAFEEQEPP EKSDPKQEES QVSGKEEETS
humsp17   EKTNFDPAEW GSKVEDRFYN NHAFEEQEPP EKSDPKQEES QISGKEEETS
rabsp17   EKTNFDPAEW GAKVDDRFYN NHAFQEHE.S EKCEA..EEK SQSVTEEETP
mussp17   EKTSFDPAEW GAKVEDRFYN NHAFKEQEQV EKCE...QEL AKSSGREETP

          101                                                150
babsp17   VTILDSS.EE DKEKEEVAAV KIQAAFRGHV AREEVKKMKT DSLQNEEKEE
humsp17   VTILDSS.EE DKEKEEVAAV KIQAAFRGHI AREEAKKMKT NSLQNEEKEE
rabsp17   VLTID.S.ED DKDKEEMAAL KIQAAFRGHL AREDVKKIRT NKAEEETEEN
mussp17   VTPFEESTEE EREQEEAAAL KIQSLFRGHV AREEVKKMKS DKNENLKEEA

          151       164
babsp17   NSEDTGFTSR THEK
humsp17   NK. . . . . .
rabsp17   N. . . . . .
mussp17   DN. . . . . .
```

FIG. 8.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FGNLLEGLTR 8
LLEGLTREIL 9
GLTREILREQ 10
REILREQPDN 11
LREQPDNIPA 12
QPDNIPAFAA 13
NIPAFAAAYF 14
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AAYFENLLEK 16
FENLLEKREK 17
LLEKREKTSF 71
KREKTSFDPA 72
KTSFDPAEWG 73
FDPAEWGAKV 21
AEWGAKVEDR 74
GAKVEDRFYN 75
VEDRFYNNHA 76
RFYNNHAFKE 77
NNHAFKEQEQ 78
AFKEQEQVEK 79
EQEQVEKCEQ 80
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QELAKSSGRE 83
AKSSGREETP 84
SGREETPVTP 85
EETPVTPFEE 86
PVTPFEESTE 87
PFEESTEEER 88
ESTEEEREQE 89
EEEREQEEAA 90
REQEEAAALK 91
EEAAALKIQS 92
AALKIQSLFR 93
KIQSLFRGHV 94
SLFRGHVARE 95
RGHVAREEVK 96
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EEVKKMKSDK 98
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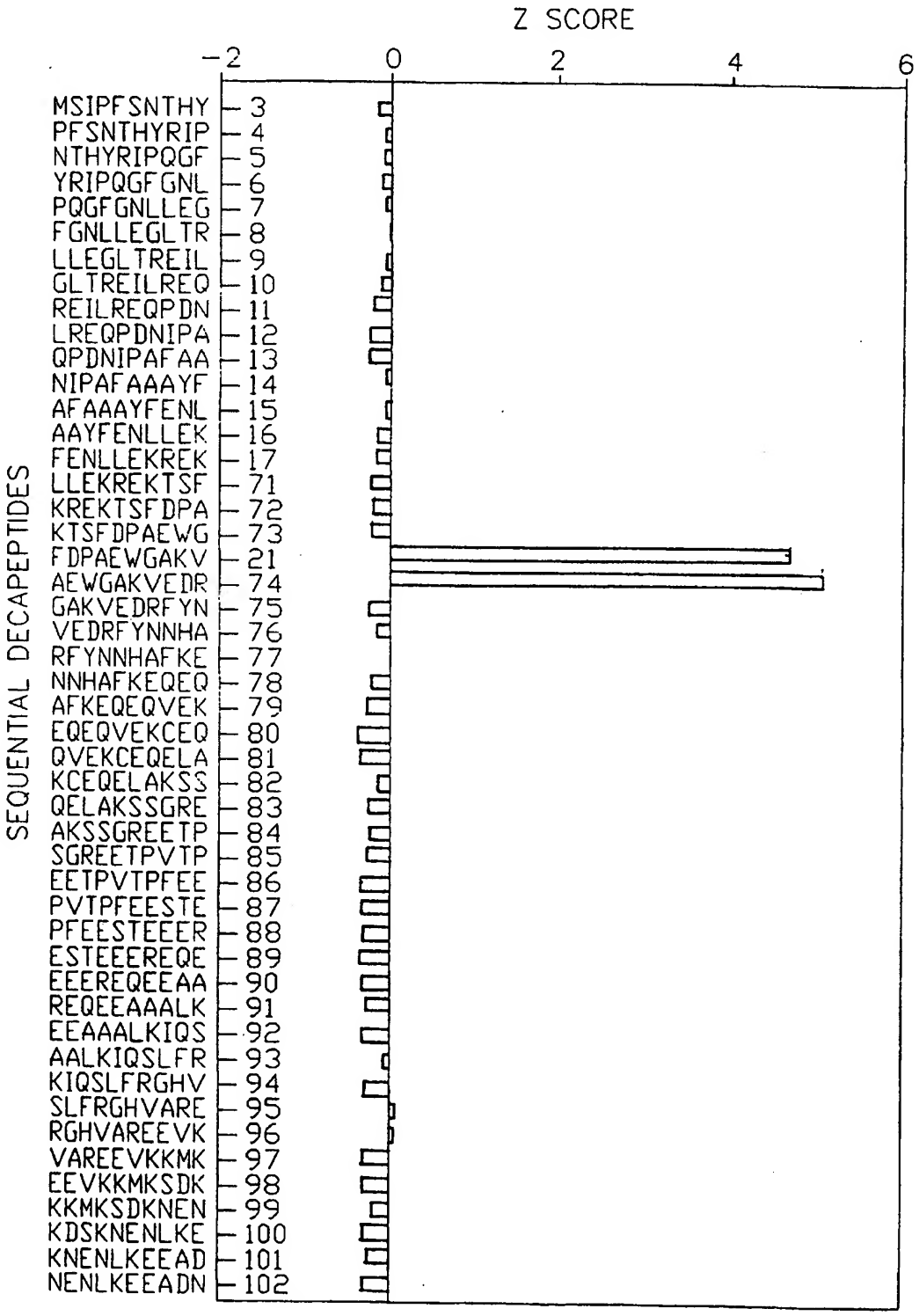
KDSKNENLKE 100
KNENLKEEAD 101
NENLKEEADN 102

FIG. 9.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FGNLLEGLTR 8
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GLTREILREQ 10
REILREQPDN 11
LREQPDNIPA 12
QPDNIPAFAA 13
NIPAFAAAYF 14
AFAAAYFENL 15
AAYFENLLEK 16
FENLLEKREK 17
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KREKTSFDPA 72
KTSFDPAEWG 73
FDPAEWGAKV 21
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GAKVEDRFYN 75
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AKSSGREETP 84
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EETPVTPFEE 86
PVTPFEESTE 87
PFEESTEEER 88
ESTEEEREQE 89
EEEREQEEAA 90
REQEEAAALK 91
EEAAALKIQS 92
AALKIQSLFR 93
KIQSLFRGHV 94
SLFRGHVARE 95
RGHVAREEVK 96
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NENLKEEADN 102

FIG. 10.

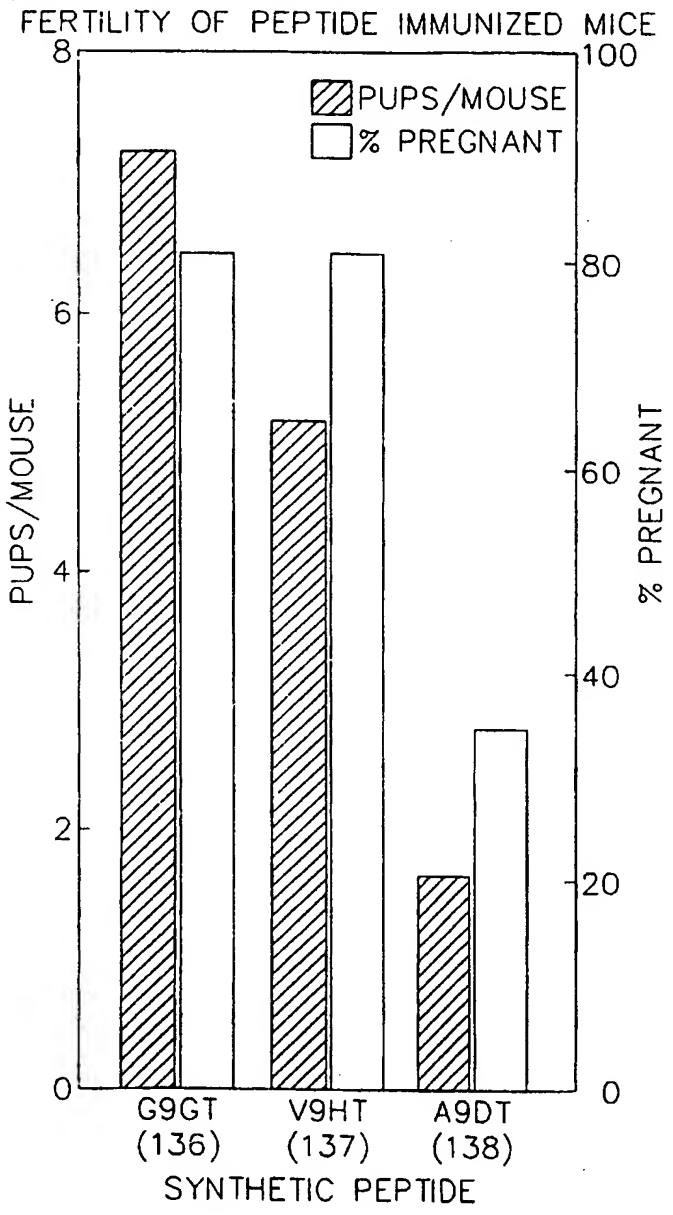
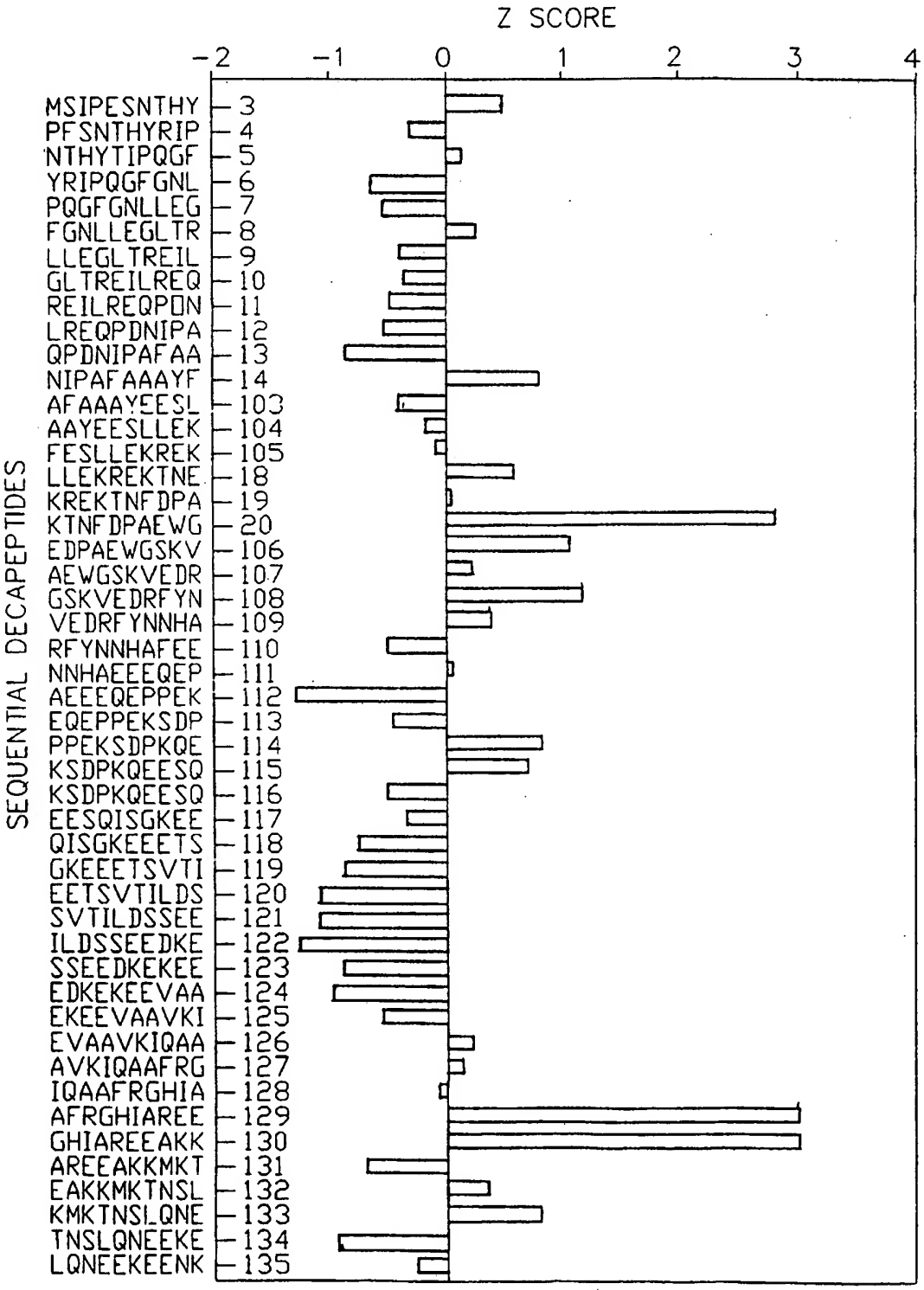

FERTILITY OF PEPTIDE IMMUNIZED MICE
PUPS/MOUSE
% PREGNANT
8
6
4
2
0
100
80
60
40
20
0
G9GT (136)
V9HT (137)
A9DT (138)
SYNTHETIC PEPTIDE

FIG. 11.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YRIPQGFGNL — 6
PQGFGNLLEG — 7
FGNLLEGLTR — 8
LLEGLTREIL — 9
GLTREILREQ — 10
REILREQPDN — 11
LREQPDNIPA — 12
QPDNIPAFAA — 13
NIPAFAAAYF — 14
AFAAAYEESL — 103
AAYEESLLEK — 104
FESLLEKREK — 105
LLEKREKTNE — 18
KREKTNFDPA — 19
KTNFDPAEWG — 20
EDPAEWGSKV — 106
AEWGSKVEDR — 107
GSKVEDRFYN — 108
VEDRFYNNHA — 109
RFYNNHAFEE — 110
NNHAEEEQEP — 111
AEEEQEPPEK — 112
EQEPPEKSDP — 113
PPEKSDPKQE — 114
KSDPKQEESQ — 115
KSDPKQEESQ — 116
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QISGKEEETS — 118
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SVTILDSSEE — 121
ILDSSEEDKE — 122
SSEEDKEKEE — 123
EDKEKEEVAA — 124
EKEEVAAVKI — 125
EVAAVKIQAA — 126
AVKIQAAFRG — 127
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GHIAREEAKK — 130
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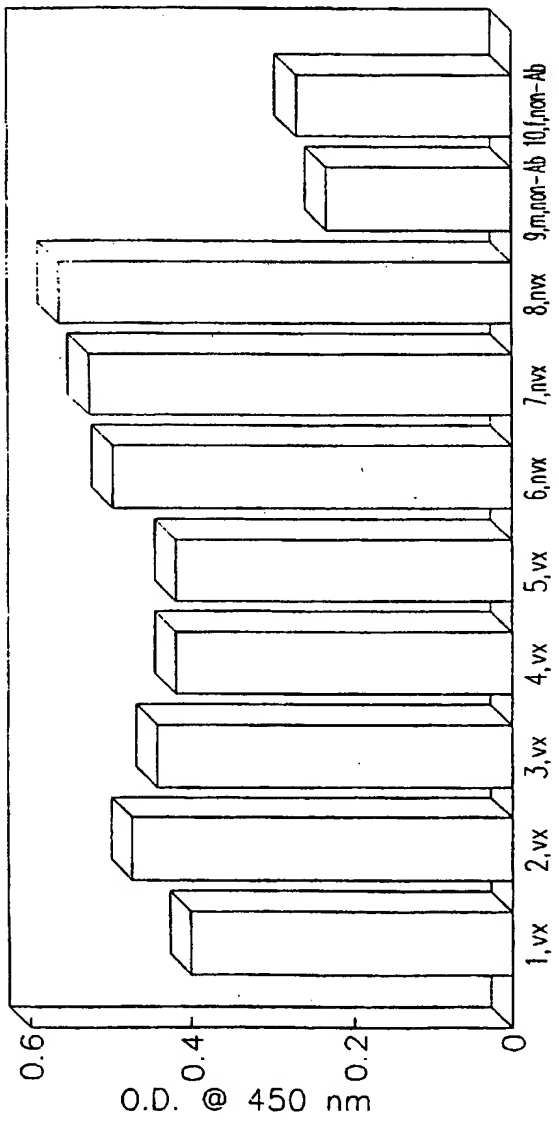
FIG. 12.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0.4
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O.D. @ 450 nm
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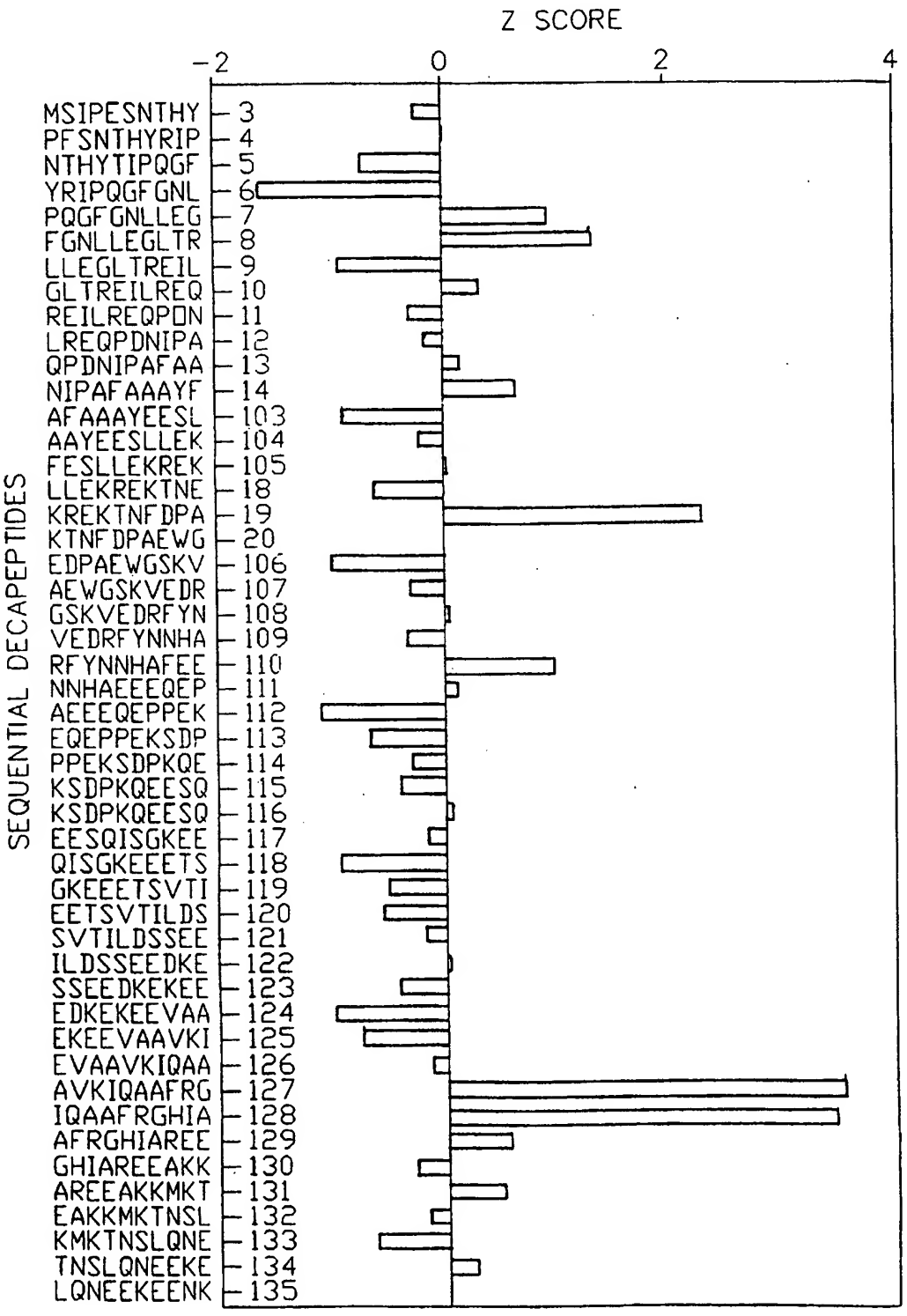
3,vx
4,vx
5,vx
6,nvx
7,nvx
8,nvx
9,m,non-Ab
10,f,non-Ab
PATIENT #

FIG. 13.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PQGFGNLLEG 7
FGNLLEGLTR 8
LLEGLTREIL 9
GLTREILREQ 10
REILREQPDN 11
LREQPDNIPA 12
QPDNIPAFAA 13
NIPAFAAAYF 14
AFAAAYEESL 103
AAYEESLLEK 104
FESLLEKREK 105
LLEKREKTNE 18
KREKTNFDPA 19
KTNFDPAEWG 20
EDPAEWGSKV 106
AEWGSKVEDR 107
GSKVEDRFYN 108
VEDRFYNNHA 109
RFYNNHAFEE 110
NNHAEEEQEP 111
AEEEQEPPEK 112
EQEPPEKSDP 113
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KSDPKQEESQ 115
KSDPKQEESQ 116
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GKEEETSVTI 119
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ILDSSEEDKE 122
SSEEDKEKEE 123
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EKEEVAAVKI 125
EVAAVKIQAA 126
AVKIQAAFRG 127
IQAAFRGHIA 128
AFRGHIAREE 129
GHIAREEAKK 130
AREEAKKMKT 131
EAKKMKTNSL 132
KMKTNSLQNE 133
TNSLQNEEKE 134
LQNEEKEENK 135

FIG. 14A.

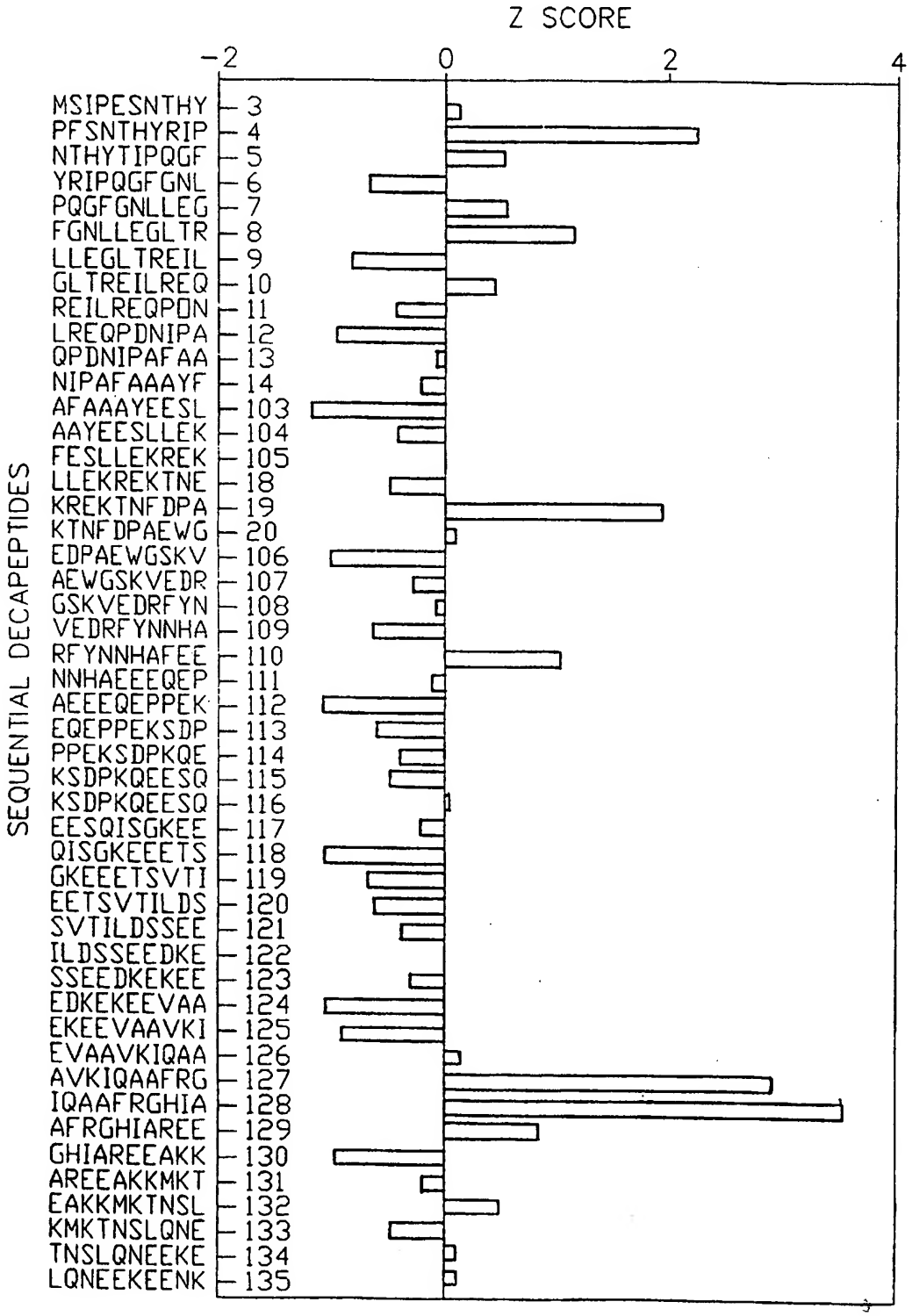
Z SCORE
−2
0
2
4
SEQUENTIAL DECAPEPTIDES
MSIPESNTHY — 3
PFSNTHYRIP — 4
NTHYTIPQGF — 5
YRIPQGFGNL — 6
PQGFGNLLEG — 7
FGNLLEGLTR — 8
LLEGLTREIL — 9
GLTREILREQ — 10
REILREQPDN — 11
LREQPDNIPA — 12
QPDNIPAFAA — 13
NIPAFAAAYF — 14
AFAAAYEESL — 103
AAYEESLLEK — 104
FESLLEKREK — 105
LLEKREKTNE — 18
KREKTNFDPA — 19
KTNFDPAEWG — 20
EDPAEWGSKV — 106
AEWGSKVEDR — 107
GSKVEDRFYN — 108
VEDRFYNNHA — 109
RFYNNHAFEE — 110
NNHAEEEQEP — 111
AEEEQEPPEK — 112
EQEPPEKSDP — 113
PPEKSDPKQE — 114
KSDPKQEESQ — 115
KSDPKQEESQ — 116
EESQISGKEE — 117
QISGKEEETS — 118
GKEEETSVTI — 119
EETSVTILDS — 120
SVTILDSSEE — 121
ILDSSEEDKE — 122
SSEEDKEKEE — 123
EDKEKEEVAA — 124
EKEEVAAVKI — 125
EVAAVKIQAA — 126
AVKIQAAFRG — 127
IQAAFRGHIA — 128
AFRGHIAREE — 129
GHIAREEAKK — 130
AREEAKKMKT — 131
EAKKMKTNSL — 132
KMKTNSLQNE — 133
TNSLQNEEKE — 134
LQNEEKEENK — 135

FIG. 14B.

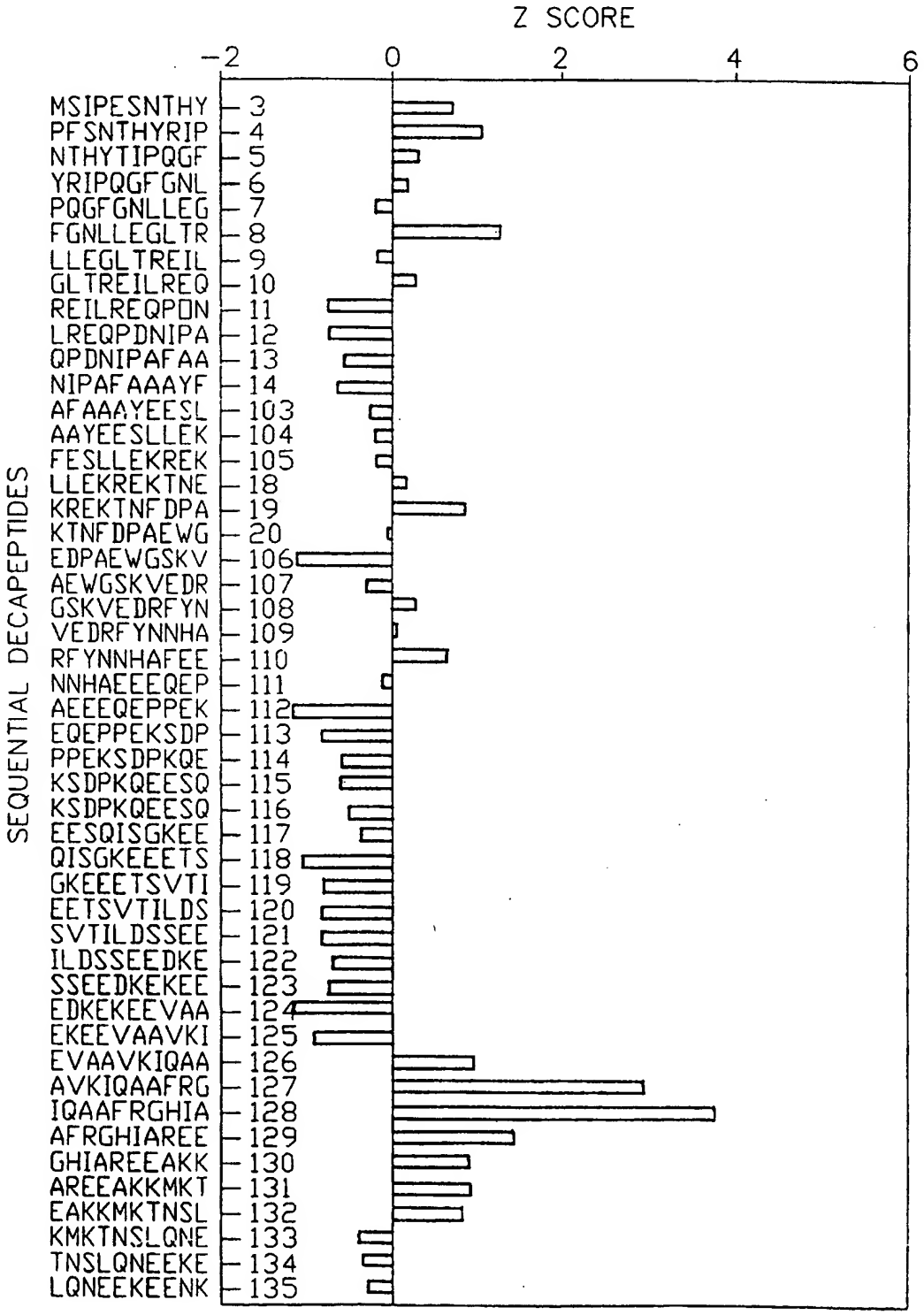
Z SCORE
−2
0
2
4
6
SEQUENTIAL DECAPEPTIDES
MSIPESNTHY − 3
PFSNTHYRIP − 4
NTHYTIPQGF − 5
YRIPQGFGNL − 6
PQGFGNLLEG − 7
FGNLLEGLTR − 8
LLEGLTREIL − 9
GLTREILREQ − 10
REILREQPDN − 11
LREQPDNIPA − 12
QPDNIPAFAA − 13
NIPAFAAAYF − 14
AFAAAYEESL − 103
AAYEESLLEK − 104
FESLLEKREK − 105
LLEKREKTNE − 18
KREKTNFDPA − 19
KTNFDPAEWG − 20
EDPAEWGSKV − 106
AEWGSKVEDR − 107
GSKVEDRFYN − 108
VEDRFYNNHA − 109
RFYNNHAFEE − 110
NNHAEEEQEP − 111
AEEEQEPPEK − 112
EQEPPEKSDP − 113
PPEKSDPKQE − 114
KSDPKQEESQ − 115
KSDPKQEESQ − 116
EESQISGKEE − 117
QISGKEEETS − 118
GKEEETSVTI − 119
EETSVTILDS − 120
SVTILDSSEE − 121
ILDSSEEDKE − 122
SSEEDKEKEE − 123
EDKEKEEVAA − 124
EKEEVAAVKI − 125
EVAAVKIQAA − 126
AVKIQAAFRG − 127
IQAAFRGHIA − 128
AFRGHIAREE − 129
GHIAREEAKK − 130
AREEAKKMKT − 131
EAKKMKTNSL − 132
KMKTNSLQNE − 133
TNSLQNEEKE − 134
LQNEEKEENK − 135

FIG. 14C.

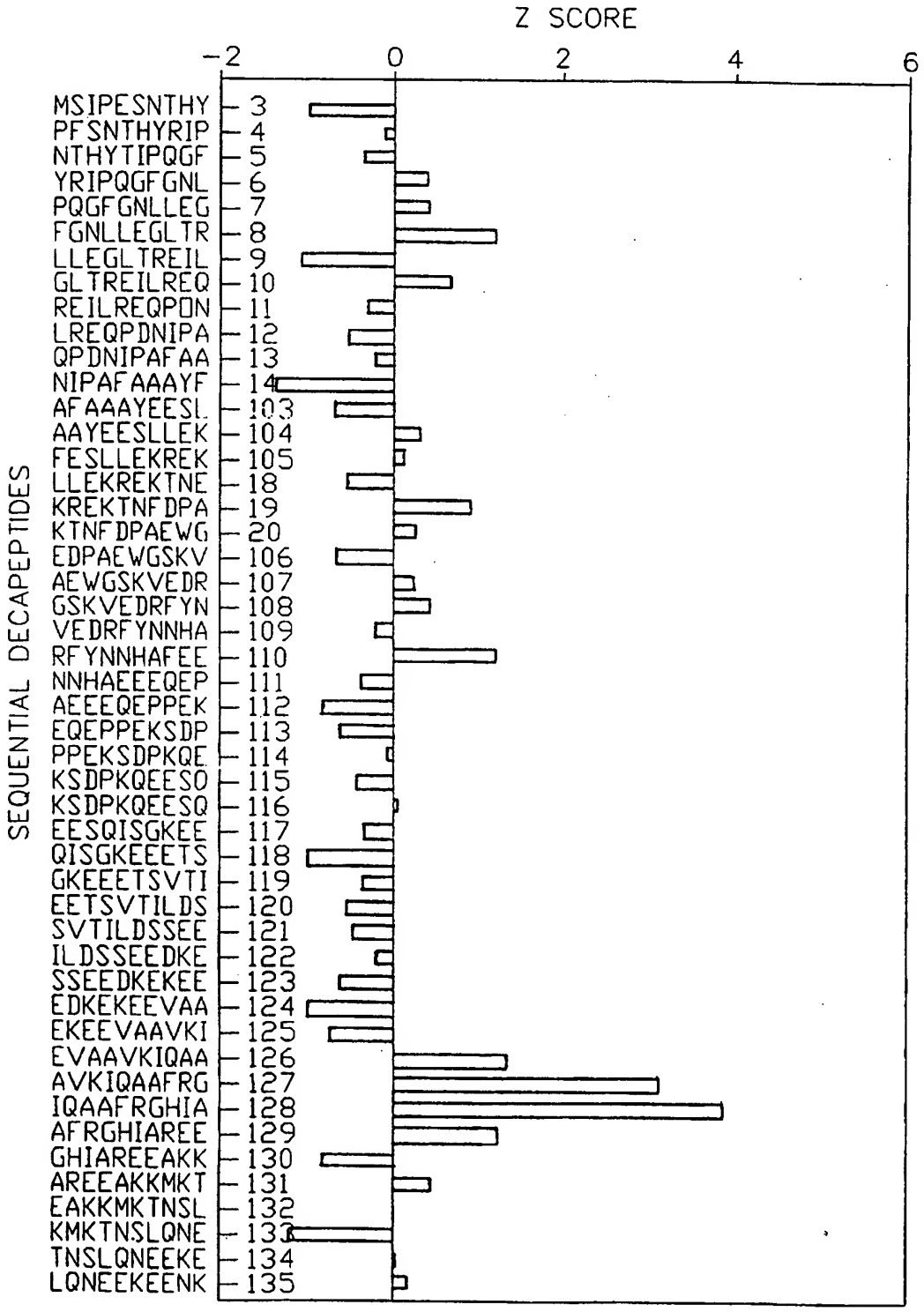
Z SCORE
−2
0
2
4
6
SEQUENTIAL DECAPEPTIDES
MSIPESNTHY — 3
PFSNTHYRIP — 4
NTHYTIPQGF — 5
YRIPQGFGNL — 6
PQGFGNLLEG — 7
FGNLLEGLTR — 8
LLEGLTREIL — 9
GLTREILREQ — 10
REILREQPDN — 11
LREQPDNIPA — 12
QPDNIPAFAA — 13
NIPAFAAAYF — 14
AFAAAYEESL — 103
AAYEESLLEK — 104
FESLLEKREK — 105
LLEKREKTNE — 18
KREKTNFDPA — 19
KTNFDPAEWG — 20
EDPAEWGSKV — 106
AEWGSKVEDR — 107
GSKVEDRFYN — 108
VEDRFYNNHA — 109
RFYNNHAFEE — 110
NNHAEEEQEP — 111
AEEEQEPPEK — 112
EQEPPEKSDP — 113
PPEKSDPKQE — 114
KSDPKQEESQ — 115
KSDPKQEESQ — 116
EESQISGKEE — 117
QISGKEEETS — 118
GKEEETSVTI — 119
EETSVTILDS — 120
SVTILDSSEE — 121
ILDSSEEDKE — 122
SSEEDKEKEE — 123
EDKEKEEVAA — 124
EKEEVAAVKI — 125
EVAAVKIQAA — 126
AVKIQAAFRG — 127
IQAAFRGHIA — 128
AFRGHIAREE — 129
GHIAREEAKK — 130
AREEAKKMKT — 131
EAKKMKTNSL — 132
KMKTNSLQNE — 133
TNSLQNEEKE — 134
LQNEEKEENK — 135

FIG. 14D.

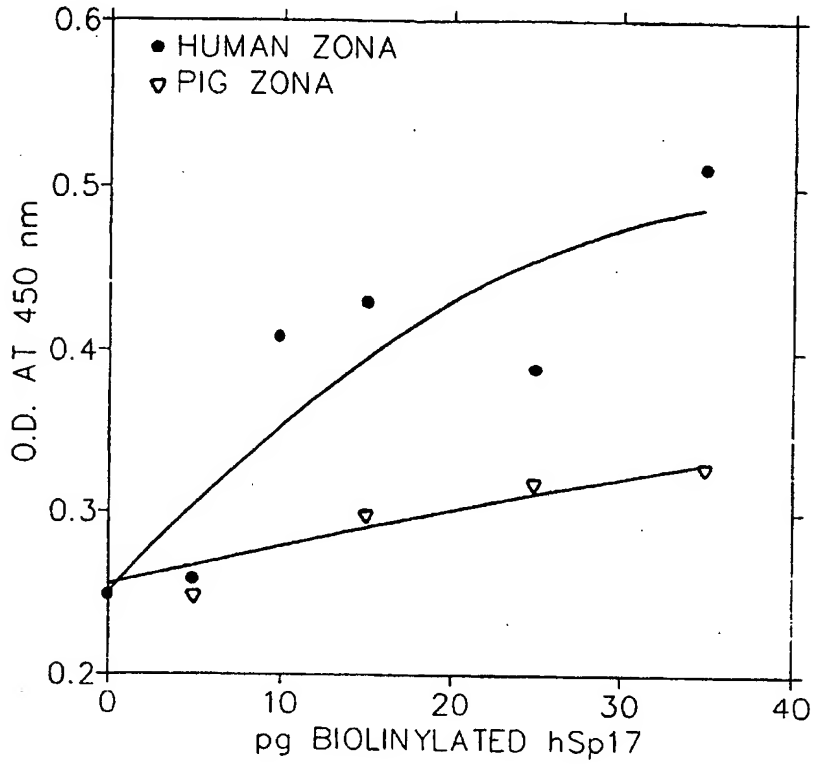
0.6
0.5
0.4
0.3
0.2
O.D. AT 450 nm
• HUMAN ZONA
▽ PIG ZONA
0
10
20
30
40
pg BIOLINYLATED hSp17

FIG. 15.

```
                                                                    1(-81)
AGCAACGAGA AAAACAACCG GAACCGGCGG CACCTGCTTG GAGAGAAAGG AGGTTCCATA -20

                                                          1(+1)
GGCAGTTCTT ACCAAGAAG ATG TCG ATT CCA TTC TCC AAC ACC CAC TAC        30
                     Met Ser Ile Pro Phe Ser Asn Thr His Tyr        10

CGA ATT CCA CAA GGA TTT GGG AAT CTT CTT GAA GGG CTG ACA CGC        75
Arg Ile Pro Gln Gly Phe Gly Asn Leu Leu Glu Gly Leu Thr Arg        25

GAG ATT CTG AGA GAG CAA CCG GAC AAT ATA CCA GCT TTT GCA GCC       120
Glu Ile Leu Arg Glu Gln Pro Asp Asn Ile Pro Ala Phe Ala Ala        40

TAT TTT GAG AGC CTT CTA GAG AAA AGA GAG AAA ACC AAC TTT GAT       165
Tyr Phe Glu Ser Leu Leu Glu Lys Arg Glu Lys Thr Asn Phe Asp        55

CCA GCA GAA TGG GGG AGT AAG GTA GAA GAC CGC TTC TAT AAC AAC       210
Pro Ala Glu Trp Gly Ser Lys Val Glu Asp Arg Phe Tyr Asn Asn        70

AAT CAT GCA TTC GAG GAG CAA GAA CCA CCT GAG AAA AGT GAT CCT       255
Asn His Ala Phe Glu Glu Gln Glu Pro Pro Glu Lys Ser Asp Pro        85

AAA CAA GAA GAA TCT CAG GTA TCT GGG AAG GAG GAA GAG ACA TCA       300
Lys Gln Glu Glu Ser Gln Val Ser Gly Lys Glu Glu Glu Thr Ser       100

GTC ACC ATC TTA GAC TCT TCT GAG GAA GAT AAG GAA AAA GAA GAG       345
Val Thr Ile Leu Asp Ser Ser Glu Glu Asp Lys Glu Lys Glu Glu       115

GTT GCT CCT GTC AAA ATC CAA GCT GCC TTC CGG GGA CAC GTA GCC       390
Val Ala Ala Val Lys Ile Gln Ala Ala Phe Arg Gly His Val Ala       130

AGA GAG GAG GTA AAG AAA ATG AAA ACA GAT AGT CTT CAa AAT GAG       435
Arg Glu Glu Val Lys Lys Met Lys Thr Asp Ser Leu Gln Asn Glu       145

GAA AAA GAG GAA AAC AGT GAG GAC ACT GGT TTT ACC TCC AGG ACA       480
Glu Lys Glu Glu Asn Ser Glu Asp Thr Gly Phe Thr SER Arg Thr       160

CAT GAA AAA TAA TCCAAATCCATCAACCTTCTTGTTAATGTCATTTTTTCCTGAG      535
His Glu Lys ***                                                  163

GAAGGAAGATTTGATGTTGTGAAATAACATTCGTTGCTGTTGTGAAAATCCGTCATGAG      594

CATTTGTTTAATAAGCATACCATTGAAACATGCCACTTGAAGATTTCTCTGAGATCATG      653
                                                 UUUUUU
AGTTTGTTTACACTTGTCTCAAGCCTATCTATAGAGACCCTTGGATTTAGAATTACAGA      712

ACAAAAGTATCTGAGATTACAGAGATCTCAGAGGTTATGTGTTTTAACCATTATCAAAT      771

GAATAAATCCTCTCTATCACATCCCAAAAAAAAAAAAAAAAAA                      816
```

FIG. 16A.

GAAGGAAGATTTGATGTTGTGAAATAACATTCGTTGCTGTTGTGAAAATCCGTCATGAG 594
CATTTGTTTAATAAGCATACCATTGAAACATGCCACTTGAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAA

FIG. 16B.

GAAGGAAGATTTGATGTTGTGAAATAACATTCGTTGCTGTTGTGAAAAAAAAAAAAA 580

FIG. 16C.

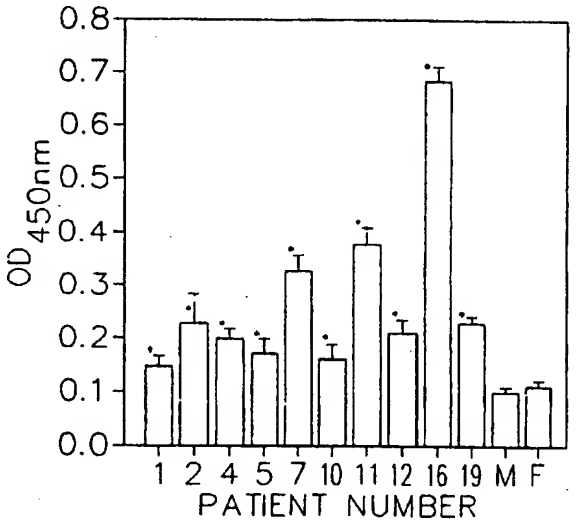

FIG. 17A.

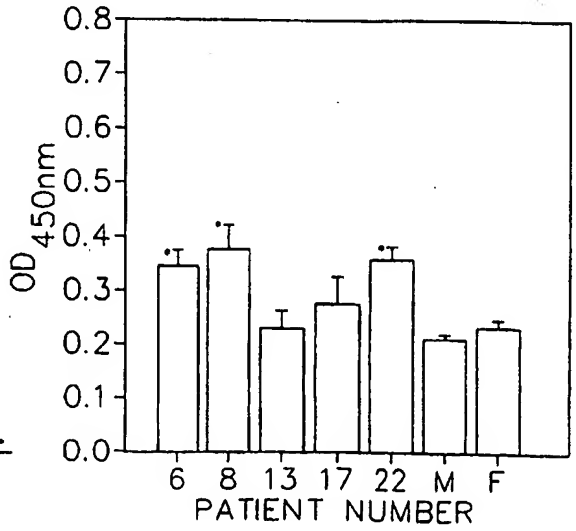

FIG. 17B.

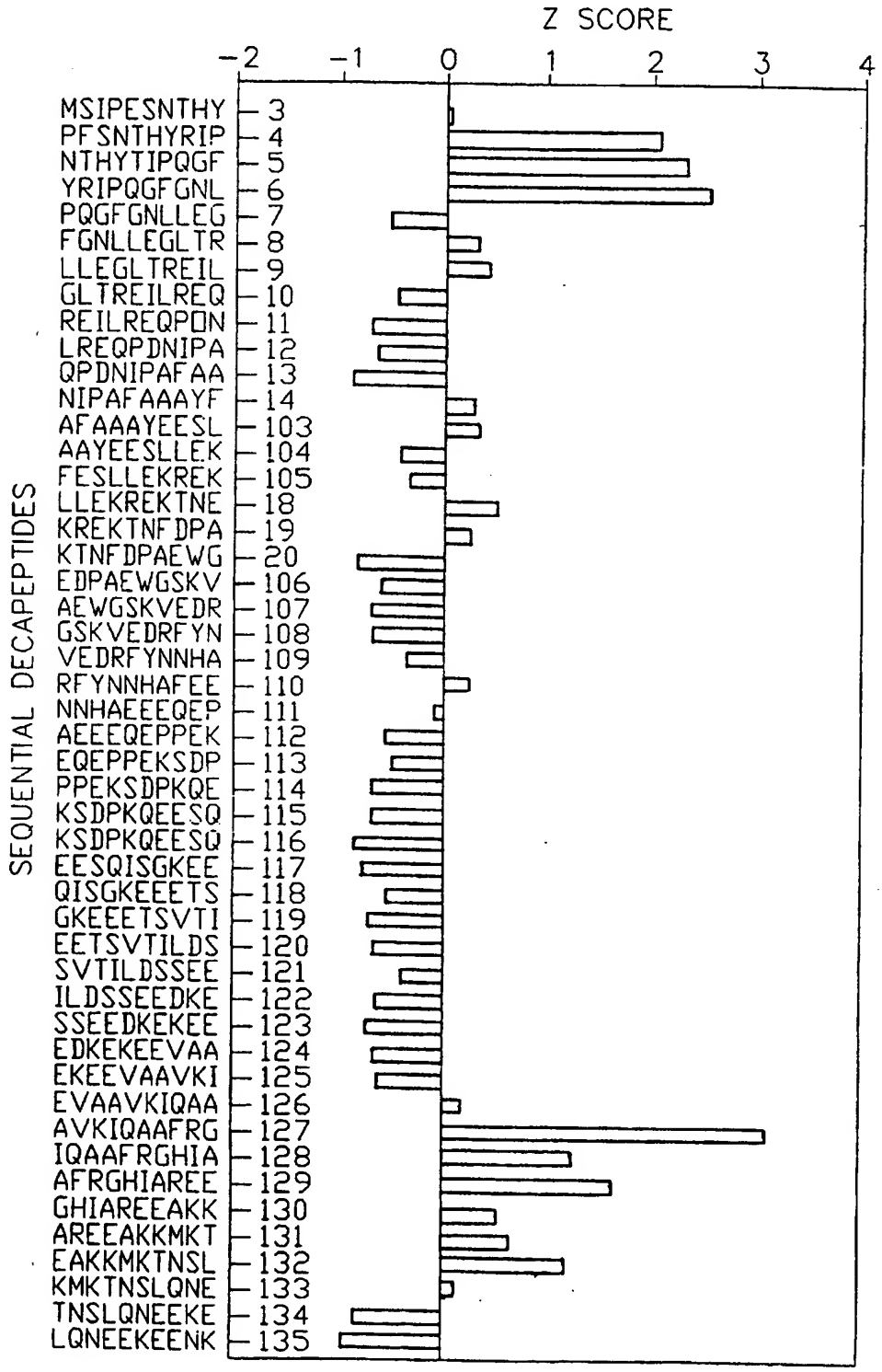
Z SCORE
−2
−1
0
1
2
3
4
SEQUENTIAL DECAPEPTIDES
MSIPESNTHY 3
PFSNTHYRIP 4
NTHYTIPQGF 5
YRIPQGFGNL 6
PQGFGNLLEG 7
FGNLLEGLTR 8
LLEGLTREIL 9
GLTREILREQ 10
REILREQPDN 11
LREQPDNIPA 12
QPDNIPAFAA 13
NIPAFAAAYF 14
AFAAAYEESL 103
AAYEESLLEK 104
FESLLEKREK 105
LLEKREKTNE 18
KREKTNFDPA 19
KTNFDPAEWG 20
EDPAEWGSKV 106
AEWGSKVEDR 107
GSKVEDRFYN 108
VEDRFYNNHA 109
RFYNNHAFEE 110
NNHAEEEQEP 111
AEEEQEPPEK 112
EQEPPEKSDP 113
PPEKSDPKQE 114
KSDPKQEESQ 115
KSDPKQEESQ 116
EESQISGKEE 117
QISGKEEETS 118
GKEEETSVTI 119
EETSVTILDS 120
SVTILDSSEE 121
ILDSSEEDKE 122
SSEEDKEKEE 123
EDKEKEEVAA 124
EKEEVAAVKI 125
EVAAVKIQAA 126
AVKIQAAFRG 127
IQAAFRGHIA 128
AFRGHIAREE 129
GHIAREEAKK 130
AREEAKKMKT 131
EAKKMKTNSL 132
KMKTNSLQNE 133
TNSLQNEEKE 134
LQNEEKEENK 135

FIG. 18.